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5. 2 AAVS5836 6. 4 AAVS5820 6. 6 ABM47321 6. 6 ABM47321 6. 6 ABM73234 6. 4 AAR36930 6. 4 AAR36930 6. 4 AAR37753 5. 6 ABU12294 5. 6 ABU123606 7. 4 AAM40200 8. 3 AAG42881 1. 3 AAG428457 8. 3 AAG42881 8. 3 AAG42881 8. 3 AAG42881 9. 5 AAE0094 9. 5 AAE00494 9. 5 AAE00494 9. 5 AAE00494 9. 5 AAE00494 9. 6 ABU18146 9. 6 ABU18136 9. 6 ABU18144 9. 6 ABU1813714 9. 6 ABU1813714	8000000000000000000000000000000000000
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GenCore versio Copyright (c) 1993 - 2005 - protein search, using sw model June 13, 2005, 13:22:36 ; S 20 29 Capop 10.0, Gapext 0.5 2105692 seqs, 386760381 res ar of hits satisfying chosen para seq length: 0 seq length: 0 seq length: 0 seq length: 2000000000 ssing: Minimum Match 0% Maximum Match 100% Listing first 300 summarie Listing first 300 summarie Listing first 300 summarie A Geneseq199906s:* 2: geneseq199006s:* 3: geneseq20008s:* 4: geneseq202002s:* 5: geneseq202003s:* 7: geneseq202003s:* 7: geneseq202003s:*	8: geneseqp2004s:* No. is the number of result by analysis of the gerived by analysis of the chert by analysis of the aderived by analysis of the chert by analysis of the
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The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzhaimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzhaimer's disease or Alzheimer's diseaserike plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzhaimer's disease. represents an inhibitor of beta-secretase enzyme.
                                                                                                                                                                                  Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
inhibitor.
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                                                                                                                                              John V,
nlogue L;
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ng S, Mcconlogue
                                            /note= "hydroxyethylene"
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Tung J, Wang S,
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                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB07872 standard; peptide; 8 AA.
                                                                                                        99US-0119571P.
                                                                                         10-FEB-2000; 2000WO-US003819
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                                                                                                                              (ELAN-) ELAN PHARM INC.
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Sinha S, Tatsuno G,
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                                                            WO200047618-A2
                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
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                               Key
Modified-site
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15-JUN-1999;
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               Synthetic
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inhibitor
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                                                            FGFR3
Ade58195
Ade58307
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Ad649093
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Aaw63844
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AAW63844
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ADO49087
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AAR21080
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ADD45446
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AAR20750
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AAE34488
ABRS6164
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ADE61700
ADF45057
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ADL61330
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ADO49089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB07871 standard; peptide; 7 AA.
14-NOV-2000
AAB07871;
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RESULT 1

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Gaps

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Sequence 68 AA;
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                                                                                                                                                                                                                                                                                                      Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taste transduction; G-protein coupled receptor; T2R; taste signaling; cAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor.
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                                                                                                                                                                                                     F, Frigon N, John V, Wang S, Mcconlogue L;
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                                                                                                                                                                                                     Doane MT,
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                                                        10-FEB-2000; 2000WO-US003819.
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99US-0139172P.
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Best Local Similarity luv...
7; Conservative
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Sinha S, Tatsuno G,
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(ADLE/) ADLER J E.
(HOON/) HOON M.
(RYBA/) RYBA N.
(MUEL/) MUELLER K.
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The invention describes an isolated taste transduction G-protein coupled receptor (1) e.g., T2R which is expressed in a taste cell, comprises greater than 60% sequence identity to a fully defined sequence of 315 (S1), 313 (S2), 299 (S1), 310 (S4), 214 (S5), 77 (S6), 209 (S7), 266 (S8), 300 (S9), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S15), 316 (S16) and 180 (S17) amino acids as given in the specification. (I) is useful for identifying a compound that modulates taste signaling in taste cells which involves contacting the compound (I). The functional effect is determined by measuring changes in intracellular cAMP, CGMP, 197, or Ca (2+). The functional effect is a chemical or physical effect. Fig. (S12), 510 (S1
                                                                                                                                                                                                                                                    Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
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Mueller K;
     Ryba N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; SEQ ID NO 80; 121pp; English.
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     Hoon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2000; 2000US-00543681
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Matches 5; Conservative
Zuker CS, Adler JE,
                                                                                            WPI; 2004-203221/19
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                                                                                                                                                        N-PSDB; ADJ84528
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The invention relates to new Proteus mirabilis polypeptides and polymerleotides. The invention also relates to antibodies against the polypeptides, amethod of generating vaccines for producing the polypeptides, amethod of polypeptides and amethod of polypeptide and a method for screening test compounds for mirabilis, a polypeptide and a method for screening test compounds for antibation activity. The polypeptides and polymerleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial dayage or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                        New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or biocontrol agents for plants.
                                                                                                                                                                                                             Disclosure; SEQ ID NO 7260; 870pp; English
                         2003-895291/82
                      WPI; 2003-895291
N-PSDB; ADF02803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 450 AA;
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Gaps ö Score 27; DB 7; Length 450; Pred. No. 1.8e+02; 0; Mismatches 1; Indels 93.1**%**; 85.7**%**; Query Match Best Local Similarity 85., 6; Conservative

VMVVAEP 292 VMXVAEF 7 286 н 셤 ઠ

ADN46338 standard; protein; 457 AA. ADN46338; RESULT 5 ADN46338

(first entry) 01-JUL-2004

Thermococcus kodakaraensis KOD1 protein sequence SeqID216.

gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.

Thermococcus kodakaraensis

WO2004022736-A1.

18-MAR-2004.

29-AUG-2003; 2003WO-IB003597

30-AUG-2002; 2002JP-00319011.

(NISC-) JAPAN SCI & TECHNOLOGY

CORP.

Imanaka T, Atomi H;

WPI; 2004-257583/24.

organism particularly analysis, applicable in genome of c Method for disrupting targeted gene in thermostable bacterium and with genome studying gene structure and functions.

Claim 9; SEQ ID NO 216; 598pp; Japanese.

This invention relates to a novel method for targeting disruption of an

whole sequential data of the genome of such organism, selecting at least larbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly thermococcus kodakaraenais KODI. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in scudying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology, with this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein concoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format diarectly from WIPO at arbitrary gene in a genome of an organism which comprises providing the ftp.wipo.int/pub/published_pct_sequences

аB aB Sequence 457 AA;

ö Score 27; DB 8; Length 457; Pred. No. 1.8e+02; 0; Mismatches 1; Indels 93.1%; 85.7%; 6; Conservative Best Local Similarity Matches 6; Conser Query Match

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Gaps

1 VMXVAEF 7 || || || VMEVAEF

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RESULT 6 ABB93074

ABB93074 standard; protein; 802 AA.

ABB93074;

(first entry) 31-MAY-2002

SEQ ID NO 2285. Herbicidally active polypeptide

Herbicidal; plant; agriculture; herbicide.

Arabidopsis thaliana

WO200210210-A2.

07-FEB-2002

28-AUG-2001; 2001WO-EP009892

28-AUG-2001; 2001WO-EP009892

(FARB) BAYER AG.

Weidler M; Tietjen K,

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms

Claim 5; SEQ ID NO 2285; 261pp + Sequence Listing; English

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

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19-JUN-2003
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Wall D,
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ID
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation required for cellular proliferation of an pathway in which a proliferation denomination of an compound 's activity; (11) a culture comprising strains in which the gene product is overexpressed (12) determining the extent to which each of the strains is present in a culture or collection of
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                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                      Gaps
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                Length 802;
                                                                     1; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #21019.
                                             93.1%; Score 27; DB 5; I 71.4%; Pred. No. 3.4e+02; iive 1; Mismatches 1;
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Yamamoto R,
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                                                                                                                                                                            ABU35492 standard; protein; 223 AA.
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0362269P.
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                Mycoplasma genitalium.
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Trawick JD,
                                                                                                                   629 VMSIAEF 635
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                                                        Local Similarity
Les 5; Conserv
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                       Sequence 802 AA;
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 herbicides
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strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo int/pub/published_pct_sequences
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(1) a vector comprising a promoter operably linked to the nucleic acid; a vector comprising a promoter operably linked by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 6; Length 223;
Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-CCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362699P.
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71.4%;
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Trawick JD,
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93 VMNIAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 223 AA;
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required for proliferation, or that inhibits callular proliferation; () required for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation or the biological pathway in which a proliferation required for callular proliferation or the biological pathway in which a proliferation required for callular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the strains or (13) identifying the candidate molecules for rational for proliferation to isolate candidate molecules for rational cortiferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence date for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained the target provery programs.
proliferation; (7) identifying a compound that influences the activity of
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89.7%; Score 26; DB 6; Length 224; 71.4%; Pred. No. 1.5e+02; ive 1; Mismatches 1; Indels
               Best Local Similarity 71.4
Matches 5; Conservative
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VMNIAEF 99
                                                             1 VMXVAEF 7
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   Query Match
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Gaps ö

ADN47550 standard; protein; 304 AA. ADN47550;

01-JUL-2004 . (first entry)

Thermococcus kodakaraensis KOD1 protein sequence SeqID1428

gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.

Thermococcus kodakaraensis.

MO2004022736-A1

29-AUG-2003; 2003WO-IB003597

30-AUG-2002; 2002JP-00319011.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Imanaka T, Atomi H;

WPI; 2004-257583/24

Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions. Claim 9; SEQ ID NO 1428; 598pp; Japanese. This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least

ransformation, and homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly Thermococcus kodakaraensis KODI. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of canced proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained the wipo.int/pub/published_pot_sequences ö Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; a vector that contains a Margetts MB; Antigenic Porphorymonas gingivalis peptides for preventing gingivitis. Gaps . 0 Length 304; Score 26; DB 8; Length 304 Pred. No. 2.1e+02; 1; Mismatches 1; Indels Patterson MA, Agius CT, Rothel LJ, Porphorymonas gingivalis protein PG21. AAY34479 standard; protein; 821 AA. 98AU-00002264. 98AU-00002911. 98AU-00003128. 98AU-00003338 98AU-00003654 97AU-00001182 98AU-00001546 Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative 98WO-AU001023 98AU-00005028 (first entry) Porphyromonas gingivalis (revised) Ross BC, Barr IG, Pa Hocking DM, Webb EA; WPI; 1999-385613/32. 41 IMKVAEF 47 1 VMXVAEF 7 N-PSDB; AAX91697 Sequence 304 AA; (CSLC-) CSL LTD WO9929870-A1. 10-DEC-1998; 27-AUG-2003 20-MAR-2003 25-AUG-1999 17-JUN-1999 10-MAR-1998 09-APR-1998 29-JUL-1998 30-JUL-1998 30-JAN-1998 23-APR-1998 05-MAY-1998 22-MAY-1998 antigenic AAY34479; RESULT 10 AAY34479 8 셤

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RESULT 12
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            AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX94583. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used to detect Porphorymonas gingivalis. Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivalis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to
                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
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                                                                                                                                Length 821;
                                                                                                                                                1; Indels
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                                                                                                                              Score 26; DB 2; 1
Pred. No. 6.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agius CT,
                                                                                                                                                                                                                                                                                                 gingivalis protein PG21.
Page 460-461; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 316-318; 588pp; English
                                                                                                                                                                                                                             AAY34354 standard; protein; 869 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson MA,
                                                                                                                              89.7%;
85.7%;
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97AU-00001182
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98AU-00005028
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                                                                                                                                                                                                                                                              (revised)
(revised)
(first entry)
                                                                                                                                        Local Similarity 85.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr IG, P
                                                                                                                                                                                   565 VMPVAEF 571
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                                                                                                                                                                 VMXVAEF
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                                                                                                              Sequence 821 AA;
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                                                                                                                                                                                                                                                                                                 Porphorymonas
                                                                                                                                                                                                                                                              27-AUG-2003
20-MAR-2003
25-AUG-1999
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Hocking DM,
                                                                                                                                                                                                                                                                                                                                                             WO9929870-A1
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29-JUL-1998
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                                                                                                                                                                                                                                                                                                                          antigenic.
                                                                                                                                                                                                                                               AAY34354;
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                                                                                                                               Query Match
                                                                                                                                                Matches
                                                                                                                                                                                                            RESULT 11
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AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                  Length 869;
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                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                               89.7%; Score 26; DB 2; I
85.7%; Pred. No. 6.7e+02;
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3800; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis polypeptide #395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH85915 standard; protein; 194 AA.
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
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Matches
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the invention fracters to an instruct acts compitating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration; (7) identifying a compound that influences the biological pathway in which a proliferation or the biological pathway is agene required for cellular proliferation or the biological pathway in which a proliferation for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the cardiac acids are useful for dentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cauged in culture of a compound. Strains in the confidention of an organism, or for screening caudidate molecules for rational cauged in confidention in cells other than S. aureus, S. typhimurium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid comprising any one of
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Xu HH;
    Gaps
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Forsyth RA,
      1; Indels
                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #14856.
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Yamamoto R,
    1; Mismatches
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                                                                                                                                                                                       ABU29329 standard; protein; 406 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00948993.
2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                                                                                        (first entry)
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis
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Trawick JD,
                                                                                  VLSVAEF 118
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                                           1 VMXVAEF 7
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25-OCT-2001;
08-PEB-2002;
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Wall D,
    Matches
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This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least a restrict and data of the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, cransformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly the genome of a hyperthermostable archaebacterium, particularly the genome of a proteins which is applicable in the genome of a gene in the genome of an organism, which is applicable in crucytion of a gene in the genome of an organism, which is applicable in crucytion of a gene at an arbitrary position in a genome can be achieved disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein crucange the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained the wipo int/pub/published_pot_sequences
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                the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; food; drug inspection; molecular biology; immunology.
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermococcus kodakaraensis KOD1 protein sequence SeqID2064
                                                                                                                                                              Length 406;
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                                                                                                                                                         Match
Local Similarity 71.4%; Pred. No. 5.3e+02;
Les 5; Conservative 1; Mismatches 1;
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                                                                           ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                       ADN48186 standard; protein; 583 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                   111 VLSVAÈF 117
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                                                                                                                                                                                                                                           1 VMXVAEF 7
                                                                                                                        Sequence 406 AA;
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Matches
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(first entry)

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; mimune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                     Human ORFX protein sequence SEQ ID NO:6058
                       ABP03038 standard; protein; 64 AA.
                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US010836.
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                                                                             24 - JUN - 2002
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                                                  ABP03038;
                                                                                                                                                                                                                                                     Ношо
            ABP03038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises beta-secretase inhibitory peptides. The beta-secretase inhibitory peptides of the invention are useful for the prevention or treatment of neurodegenerative diseases, such as:
Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis, cerebral palsy, and memory loss. The beta-secretase inhibitory peptides of the invention are also useful in the manufacture of an sAPPR secretion promoter or neurotropic factor-like agent. The present amino acid sequence represents a beta-secretase inhibitory peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compound such as beta-secretase inhibitor, useful as preventive or therapeutic agent for treating neurodegenerative disease such as Alzheimer's disease, Parkinson's disease and neuropathy.
                                                                                                                                                                                                                                                                                       beta-secretase inhibitory peptide; neurodegenerative disease;
Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
cerebral palsy; memory loss; AAPPA secretion promoter;
neurotropic factor-like agent.
                                                                  Gaps
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                                     86.2%; Score 25; DB 8; Length 583; 71.4%; Pred. No. 7.9e+02;
                                                               1; Indels
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                Beta-secretase inhibitory peptide - SEQ ID 70.
                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                    ADS09499 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2004; 2004WO-JP002438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003; 2003JP-00052926.
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6; Conservative
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439 VMAVAEY 445
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                                                Local Similarity
            Sequence 583 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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Best Local &
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Matches
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27525 encode the human ORFX proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a cyndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders allitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic corpus systhematosus, hypertension, hypothyroidism, cholesterol ester corpus storage diseases, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host conservative conservative diseases. On the conservative diseases of the conservative diseases of the conservative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating burns, inclisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from restemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                            Disclosure; SEQ ID NO 6058; 1037pp; English.
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uvaitis; endopthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; engryme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhatia A;
                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #17674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 17973; 1069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW, Persing DH, Mitcham J
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                   AAUS6778 standard; protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-0199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                              (first entry)
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes
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                                  VMDVAEY 59
1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS59578
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200181581-A2
                                                                                                                                                                                                                 27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001.
                                    23
                                                                                                                                                                          AAU56778;
                                                                                            RESULT 17
                                                                                                                AAU56778
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Gaps

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Score 24; DB 4; Length 75; Pred. No. 1.6e+02; 0; Mismatches 2; Indels

82.8%;

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The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (BMB35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polymeptide of the invention; an proteins comprising a polypeptide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polymeleotides, a vaccine composition (comprising P acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit confident; and a method for inhibiting the development of P. acnes in a patient; The P. acnes polypeptides, polymeleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymeptides are useful for diagnosing, preventing or treating acne protein. The polymulations or antigen-presenting cells that express the polymeptides are useful for diagnosing, preventing or treating acne protein. The polymulations or antigen-presenting cells that express the protein. The polymulations and also be used as probes or primers for uncleic acid hybridistation. The vaccine composition is useful for the esquence represents a polypeptide predicted to be encoded by an ORF (open ceducing frame) contained within the P. acnes polymucleotides of the cinvention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the printed specification, but an immune the polyment of the printed specification, but an immune the polyment of the printed specification, but an immune the polyment of the printed specification, but an immune the polyment of the printed specification, but an immune the pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #17973.
                                                                                                                                                                                                                                                                                                                                                                 Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 17973; 1481pp; English
                                                                                                                                                                  ABM53297 standard; protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, Skeiky YAW, Pers:
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2002; 2002WO-US032727.
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                                                                                                                                                                                                                                                                 20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes.
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1 VMXVAEF 7
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                                        VMAVCEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; SPTM, autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; halzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipportatic; antianaemic; anti-HVV; human immunodeficiency virus; secretory polynucleotide; secretory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu JY, Tuason O, Yap PE, Amshey SR;
Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Lewis SA, Chen AJ, Panzer SR, Harris B;
Lo A, Lan RY, Urashka ME;
                                                                          Gaps
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  Score 24; DB 6; Lengtn 73, Pred. No. 1.6e+02;
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), Yap PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secretory polypeptide SPTM SEQ ID NO 770.
                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                         ABP75586 standard; protein; 97 AA.
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29-WAR-2001; 2001US-0280068P.
17-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291839P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-029448P.
20-JUN-2001; 2001US-029476P.
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                       82.8%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                       5; Conservative
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Daughtery SC, Dam TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peralta CH, David MH
Flores V, Marwaha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-075543/07.
                       Query Match
Best Local Similarity
                                                                                                                             VMXVAEF
                                                                                                                                                                               VMAVCEF
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                                                                          Matches
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Zhao QA;
disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cervix or prostate). The present sequence is one of the SpTM proteins of the invention (ABP75384-ABP75962). Note: The sequence data for this patent did not form part of the printed specfication, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAIS7798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                        Gaps
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Zhang J,
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Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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Yang Y,
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Xue AJ,
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                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAM41985 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 6916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00471275.
2000US-0048B725.
2000US-00552317.
2000US-00598042.
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2000US-00653450.
2000US-00662191.
2000US-00693036.
                                                                                                                                                                                                                                       82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                        5; Conservative
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Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442253/47.
N-PSDB; AAI61141.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                     2 MXVAEF 7
                                                                                                                                                                                                      Sequence 97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
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03-AUG-2000;
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Zhou P,
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Matches
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           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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                                                 system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzeimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolypic activity, chemotactic/chemokinetic activity, haemostatic as the and thrombolypic activity, ancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humanostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J, Zhao
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                                                                                                                                                                                                                             82.8%; Score 24; DB 4; Length 132; 71.4%; Pred. No. 2.9e+02; ive 1; Mismatches 1; Indels
encoded polypeptides (AAM38642-AAM42213) with nootropic,
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Yang Y,
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Xue AJ,
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rman T, Xu C,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                AAM41986 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 6917.
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21-JAN-2000; 2000US-00488725.
25-AFR-2000; 2000US-00552117.
20-UUN-2000; 2000US-00598042.
19-UUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
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Wang Z, Wehrman T
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                            Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
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Goodrich R,
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LMVVAEF 70
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                                                                                                                                                                                                     Sequence 132 AA;
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Wang J,
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Zhou P;
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

WPI; 2001-442253/47.

N-PSDB; AAI61142

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                                                                     The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as parkinson's disease, injuries, peripheral nervous system disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, activities and inflammation, leukaemias and State and Control activity, atthritis and inflammation, leukaemias and control activity, atthritis and inflammation, leukaemias and control activity, atthritis and inflammation, leukaemias and control activity, activity a
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Zhang J, Zhao QA;
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Pred. No. 2.9e+02;
1; Mismatches 1; Indels
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Yang Y,
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Xue AJ,
Example 2; SEQ ID NO 6917; 10078pp; English.
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              part of the printed specification
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25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
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03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653191.
19-OCT-2000; 2000US-00653036.
29-NOV-2000; 2000US-00727344.
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71.4%;
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N-PSDB; AAI61140.
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Best Local Similarity
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Wang J, 1
Zhou P, 0
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytoatatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous is system, such as peripheral nervous injuries, peripheral nervous contained nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic laterial selectorsis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, chemotextic/chemokinetic activity, hammostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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Novel nucleic acids and polypeptides, useful for treating disorders such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 4; Length 132; 71.4%; Pred. No. 2.9e+02; ive 1; Mismatches 1; Indels
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                                                                                             Example 2; SEQ ID NO 6915; 10078pp; English.
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                                      as central nervous system injuries.
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22-MAR-2001; 2001US-0278013P.
30-MAY-2001; 2001US-0294394P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200246392-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG98409;
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IID ABG9

IID ABG9

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This invention relates to a three dimensional structure of Thermus thermophilus 70S ribosome resolved using x-ray crystallography up to 5.5

Disclosure; Page 502; 525pp; English.

Novel three dimensional structure of Thermus thermophilus 70S ribosome resolved using x-ray crystallography upto 5.5 Angstroms resolution, useful for screening and designing compounds that alter ribosome

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Angstrom resolution. The invention also discloses a method for identifying a compound that binds to a bacterial 70S ribosome or its portion. The method comprises designing a compound based upon a three-dimensional structure of the bacterial 70S ribosome, where the structure co-ordinates are given in the specification, contacting the compound with the bacterial 70S ribosome or its portion and determining whether the compound binds to the bacterial 70S ribosome or its portion. The 70S ribosome is sites on the new or its portion. The 70S ribosome is sites on the 70S ribosome and design compounds that bind to sites on the 70S ribosome and that alter the ribosome function. The present sequence represents a ribosomal protein sequence used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(11 a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated applypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                            Score 24; DB 5; Length 145; Pred. No. 3.2e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #10141.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 52538; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU24614 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                              82.8%;
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-029926/02
                                                                                                                                                                                                                                                                                                                                        2 MXVAEF 7
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                                                                                                                                                                                                                            Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                            1 MSVAEF
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06-SEP-2001;
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08-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU24614;
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU24614
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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fits.
                           the gene product or that has an activity against a biological pathway identifying a gene required for callular proliferation; (8) identifying a gene required for callular proliferation or the biological pathway in which a proliferation-required men or the biological pathway in which a proliferation-required men or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for callular proliferation to isolate candidate molecules for rational
proliferation; (7) identifying a compound that influences the activity of
$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 191 AA;

82.8%; Score 24; DB 6; Length 191; 57.1%; Pred. No. 4.3e+02; ive 2; Mismatches 1; Indels Query Match
Best Local Similarity 57.1
Matches 4; Conservative 131 LMAIAEF 137 1 VMXVAEF 7 셤 8

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Gaps

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RESULT 25 ABU23979 ABU23979;

ABU23979 standard; protein; 195 AA.

(first entry) 19-JUN-2003

Protein encoded by Prokaryotic essential gene #9506.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Clostridium acetobutylicum.

WO200277183-A2

03-OCT-2002

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851.

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02. N-PSDB; ACA27849 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 51903; 1766pp; English.

the inventor relates to an insolated muchalc acid compilating any one or the inventor relates to an insolated muchalc acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co of the nucleic acid inhibits proliferation of a cell. Also included are:

Co encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide, (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) dentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture compusing strains in which the each of the strains is present in a culture or collection of compound's activity; (11) a culture compising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for dentifying proteins or screening for homologous mucleic acids required for cellular proliferation of an organism. The antisense mucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for cellular proliferation of solate candidate molecules for rational ö drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from NIPO at from the proposition of the printed specification. Gaps 82.8%; 57.1%; Query Match Best Local Similarity 57.1%, Best Local Similarity 4; Conservative Sequence 195 AA;

ö Score 24; DB 6; Length 195; Pred. No. 4.4e+02; 2; Mismatches 1; Indels

131 LMAIAEF 137 1 VMXVAEF

ò g RESULT 26

ADJ48536 standard; protein; 195 AA. ADJ48536; ADJ48536

06-MAY-2004 (first entry)

Oil-associated gene related protein #36.

oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

Unidentified.

JS2004025202-A1.

05-FEB-2004.

14-MAR-2003; 2003US-00389566.

15-MAR-2002; 2002US-0365301P. 26-JUN-2002; 2002US-0391786P. 26-JUN-2002; 2002US-0392018P.

LAURIE C C. RAVANELLO M. LAUR/) RAVA/)

SAVAGE T. LEDEAUX J R. (SAVA/) (LEDE/) (ROGE/)

ROGERS J A.

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                                                                                                                                                                     promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-Z96494) and their encoded proteins (see AAX961792.Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of
                                                             Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae proteins and related DNA - useful for screening
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention; disease; diagnosis; gene therapy; screening; antimicrobial; antibiotic; pathogenesis; infection.
                                                                                                                                                         The invention relates to a recombinant DNA construct comprising a
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 Rogers JA;
                                                                                                                                                                                                                                                                                                                                             Length 195;
                                                                                                                                                                                                                                                                                                                               Score 24; DB 8; Length 155, Pred. No. 4.4e+02;
   Ledeaux JR,
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                           Example 3; SEQ ID NO 540; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 338-339; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae proteins and compounds for antibacterial activity
 Savage T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY85820 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. pneumoniae derived protein #29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0024022P.
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                                                                                                                                                                                                                                                                                                                                               82.8%;
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Best Local Similarity 71.**,
Best Local Si Conservative
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 Ravanello M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-159452/14.
                              WPI; 2004-142683/14
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                                                                                                                                                                                                                                                                                                                Sequence 195 AA;
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                                                                                          Beed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment;
bacterial;
Laurie CC,
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                                                                                            plant
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such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
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                                                                                                                                                                                                                Length 225;
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                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein #11698.
                                                                                                                                                                                                              82.8%; Score 24; DB 2; Le: 71.4%; Pred. No. 5.1e+02; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological; osteopathic; neuroprotectant.
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, Jen S, Carter D;
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                                                                                                                                   infection, dysfunction and disease
                                                                                                                                                                                                                                                                                                                                                                                                                           AAU50802 standard; protein; 236
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2001; 2001WO-US012865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                Best Local Similarity 71.4
Matches 5; Conservative
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e J, Zhang 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                             115 VMSAAEF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                        1 VMXVAEF
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                                                                                                                                                                            Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU50802;
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                       AAU50802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a Propionibaccerium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ARM35624-ARM64536) and to additionally encompassof P. acnes polypeptides. The invention additionally encompasson vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; an importance specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #11997,
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                              Score 24; DB 4; Length 236;
Pred. No. 5.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 11997; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM47321 standard; protein; 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                    82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                      71.48;
                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 71.**,
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                    || :|||
VMELAEF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-381789/36.
N-PSDB; ACF64478.
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                                                                                                                                                                                                                                                                                            1 VMXVAEF
                                                                                                                                                                               Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2003
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                                                                                                                                                                                                                                                                                                                                  169
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ABM47321
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proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnewulgaris, or for stimulating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated appropptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                                                                                                                                                                Length 236;
                                                                                                                                                                                                                                                                                                                                  1; Indels
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Forsyth |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #11793.
                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 6; I
71.4%; Pred. No. 5.4e+02;
iive 1; Mismatches 1;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 54190; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU26266 standard; protein; 238 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0372851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                169 VMELAEF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                           Sequence 236 AA;
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Wall D,
                                                                                                                                                                                                                                                                                              Query Match
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proliferation or the activity of a gene in an operon required for the proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains in collidar inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proceins or screening for homologous nucleic acids required for interface and a proliferation of a compound that inhibits for identifying proceins or screening for homologous nucleic acids required for interface and processed or the indicate molecules for retional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; includaton conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 786; 1755pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY36930 standard; protein; 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-371125/31.
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VLSIAEF 78
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 AA;
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04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY36930;
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AC AAY3

XX AAY3

XX AAY3

XX AAY3

XX VACC

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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as

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vaccines against Chlamydia trachomatis. Antisense and ribozyme sequent can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, peritypeptitis, bartholinitis; pneumopathy in breast feeding infants; wenereal lymphogranulomatosis. The polypeptides of the invention may be use in treating these diseases
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                Score 24; DB 2; Length 254; Pred. No. 5.8e+02; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 48693; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #18325.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG18334 standard; protein; 286 AA.
                                                                                                                                                                                                                              82.8%;
71.4%;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                       5; Conservative
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VMIVADF 12
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Best Local Similarity
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N-PSDB; AAS82521.
                                                                                                                                                                                                                                                                                                          1 VMXVAEF
                                                                                                                                                                                               Sequence 254 AA;
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated binding pocket of receptor tyrosine kinase that regulates the kinase domain of the receptor, useful for identifying modulator of the receptor for treating lymphoproliferative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor tyrosine kinase; RTK; kinase domain; cytostatic; antiarthritic; antiinflammatory; immunosuppressive; antirheumatic; virucide; noctropic; neuroprotective; cerebroprotective; antiparkinsonian; dermatological; nephrotropic; tranquilizer; vulnerary; anticonvulsant; VAB-1.
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                    Length 286;
                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                  Score 24; DB 4; I
Pred. No. 6.6e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                      ABB81185 standard; protein; 332 AA
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                                                                                                                                                                                  y Match
Local Similarity 71.4%;
hes 5; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAB-1 protein sequence.
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                                                                                                                                                  Sequence 286 AA;
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       make a model for (1) or its complexes or parts, in First procest, to make a model for (1) or its complexes or parts, in First orpystallography techniques, or for determining three-dimensional structures of polypeptides with unknown structures. Pharmaceutical compositions comprising the ligand or modulator is useful for tracting lymphoproliferative conditions, malignant and pre-malignant conditions lymphoproliferative conditions, malignant and pre-malignant conditions lupus erythematosus, immune-related glomerulonephritis, rheumatoid arthritis), viral infection, inflammation, graft versus host disease, neurodegenerative diseases and conditions involving trauma and injury to Huntington's disease and multiple sclerosis). The present sequence represents a VAB-1 protein sequence
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae cellular proliferation protein #182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                           Length 332;
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Pred. No. 7.8e+02;
1; Mismatches 1; Indels
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26-WAY-2000; 2000US-0207777P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
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                                                                                                                                                                                                                                                                         similarity 71.4%;
5; Conservative
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Xu HH;
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Best Local Similarity
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                                                                                                                                                                                                                                          Sequence 332 AA;
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Yamamoto RT,
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Matches
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useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 335 AA;
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Length 335;
  Score 24; DB 4; Lengua compred, No. 7.9e+02; Triches 2; Indels
                                 0; Mismatches
            82.8%;
Query Match
Query Match
Bost Local Similarity 71.40,
Bost Local Similarity 71.40,
                                                                             224 VMSAAEF 230
                                                      1 VMXVAEF 7
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Gaps .. 0

RESULT 35

S. pneumoniae type 4 strain protein from coding region #869. ABU01294 standard; protein; 335 AA. (revised)
(first entry) 23-OCT-2003 11-FEB-2003 ABU01294; ABU01294

Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.

Streptococcus pneumoniae; type 4 strain.

WO200277021-A2.

03-OCT-2002.

27-MAR-2002; 2002WO-IB002163.

27-MAR-2001; 2001GB-00007658.

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

Masignani V, Tettelin H, Fraser C;

WPI; 2003-040579/03. N-PSDB; ABX06581 New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or infection

Claim 1; SEQ ID NO 1738; S6pp; English.

The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56494. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a

cc sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence to the target sequence and the second primer is substantially complementary to the complement of the target sequence to substantial complementarity define the terminio of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes concoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences. (Updated on 23-OCT-2003 to

Sequence 335 AA;

ö Gaps ; 0 Score 24; DB 6; Length 335; Pred. No. 7.9e+02; 0; Mismatches 2; Indels 0; Mismatches 82.8%; 71.4%; Best Local Similarity 71.4 Matches 5; Conservative Query Match

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ABP81576 standard; protein; 335 AA. ABP81576; RESULT 36 ABP81576

Streptococcus pneumoniae polypeptide SEQ ID NO 654. (first entry) 04-MAR-2003

Streptococcus pneumoniae; infection; otitis media; antibacterial; diagnosis; gene therapy.

Streptococcus pneumoniae

WO200283855-A2.

24-OCT-2002

L2-APR-2002; 2002WO-US011524.

16-APR-2001; 2001US-0283948P.

(AMCY) AMERICAN CYANAMID CO

Russell DP; Chakravarti DN, Zagursky RJ, Masi AW, Green BA, Wooters JL;

WPI; 2003-093010/08.

N-PSDB; ABZ42424.

preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. New Streptococcus pneumoniae polynucleotides, useful for treating

Claim 42; Page 921-923; 1091pp; English

당 The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) a Streptococcus pneumoniae genomic sequence, a fragment or degenerate

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABPB1299-ABPB1674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for pneumoniae in a biological sample or diagnosing S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                         Score 24; DB 6; Length 335;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #31517.
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                                                                                                                                                                                                                                               0; Mismatches
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                                                                                                           82.8%;
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Best Local Similarity 71.40,
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Trawick JD,
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                                                                                                                                                                       Sequence 335 AA;
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Wall D,
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pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. T. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Mote: The sequence data for this ferred in collection, but was obtained the collection of form part of the printed specification, but was obtained the collection of the collection of the printed specification, but was obtained the collection of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
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0; Mismatches 2; Indels
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98US-0085131P.
98US-00107433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 71.4%;
5; Conservative
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Matches 5, Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 335 AA;
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12-JUL-1999;
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04-AUG-1999;
04-AUG-1999;
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16-JUL-1
   ö
Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this parent did not appear in the printed specification but was obtained in electronic format directly from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                           Score 24; DB 8; Length 335;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 23321
                                                                                                                                                                                                                                                                                                                            AAG20945 standard; protein; 361 AA
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99US-0127462P

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99US-0128445P

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99US-0131449P

99US-0132484P

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99US-0136392P.
99US-0136782P.
                                                                                                                         Query Match
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                                                                                          Sequence 335 AA;
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121-APR-1999

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150-MAY-1999

160-MAY-1999

170-MAY-1999

180-MAY-1999

190-MAY-1999

190-MAY-1999
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RR 06-AUG-1999 9918-0141362P

RR 10-AUG-1999 9918-014431P

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RR 20-AUG-199
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
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82.8%;
ilarity 71.4%;
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Matches 5; Conserv
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Query Match
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	Gaps	
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	Length 361; ; Indels	
	DB 3; Le 8.5e+02; ches 1;	
	24; No. mat	
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23 - 70N - 1999;
24 - 70N - 1999;
26 - 70N - 1999;
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09-AUG-1999;
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11-AUG-1999;
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17-AUG-1999;
18-AUG-1999;
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03-AUG-1999;
04-AUG-1999;
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9905-0126264P.
9905-0127462P.
9905-0127462P.
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99US-0131449P.
99US-0132048P.
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99US-0134256P.
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                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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05 - MAR - 1999

23 - MAR - 1999

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10 - APR - 1999

11 - APR - 1999

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                         RESULT 41
                                             AAG2458

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                     Protein encoded by Prokaryotic essential gene #9133.
                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 51530; 1766pp; English.
                                                                                                                         06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                 21-MAR-2001; 2001US-00815242.
                                                                                                  21-MAR-2002; 2002WO-US009107
                                                                                                                                                 06-MAR-2002; 2002US-0362699P
                                                   Clostridium acetobutylicum
       19-JUN-2003 (first entry)
                                                                                                                                                                ELIT-) ELITRA PHARM INC.
                                                                                                                                                                              Wang L, Zamudio C,
Wall D, Trawick JD,
                                                                                                                                                                                                      WPI; 2003-029926/02
                                                                                                                                                                                                               N-PSDB; ACA27476.
                                                                    WO200277183-A2
                                                                                  03-OCT-2002.
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9905-0159330P.
9905-0159331P.
9905-0159631P.
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99US-0161405P.
99US-0161406P.
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99US-0161361P.
99US-0161920P.
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99US-0161993P.
99US-0162142P.
                                                    99US-0151065P.
99US-0151066P.
99US-0151080P.
       99US-0149723P.
99US-0149929P.
99US-0149930P.
99US-0149930P.
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                                                                                                                          99US-0154018P.
                                                                                                                                         99US-0154779P.
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                                    99US-0150566P.
                                                                           99US-0151303P.
                                                                                                    99US-0152363P.
                                                                                                          99US-0153070P.
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                                                                                                                                                                         99US-0156458P
                                                                                           99US-0151930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                             12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                        28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
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21-OCT-1999;
22-OCT-1999;
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22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
                              23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
                                                                    27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
                                                                                                  07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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14-0CT-1999;
                                                                                                                                                                                                                       08-OCT-1999;
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21-OCT-1999,
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                                                     27-AUG-1999;
27-AUG-1999;
                                                                                                                                         20-SEP-1999
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28-OCT-1999
                                                                                                                          15-SEP-1999
16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Zyskind JW; Xu HH;

Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA,

Malone C, Carr GJ,

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the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense continued acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contisense or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway continued for proliferation or the biological pathway in which a proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling the extent compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or product is overexpressed or underexpressed; (12) determining the extent of strains; or (13) identifying the target of a compound that inhibits the conjusting proteins or screening for homologous nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for the proversor proverse or andidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification of the printed from wipo int/pub/published_pct_sequences
The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 6; Length 367 ilarity 71.4%; Pred. No. 8.7e+02; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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ABU23606 standard; protein; 367 AA.

RESULT 42 ABU23606 ID ABU23 XX AC ABU23

ABU23606;

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Gaps

; 0

Indels

1;

AAM40200 ID AAM

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hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 23320.
 Pred. No. 8.8e+02;
                1; Mismatches
                                                                                                                                                               AAG20944 standard; protein; 378 AA.
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99US-0123180P.
99US-0125788P.
99US-0125784P.
99US-0125785P.
99US-0127452P.
99US-0128234P.
99US-0128234P.
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99US-0130449P.
99US-013049P.
99US-0131449P.
99US-0132448P.
99US-0132484P.
99US-0132484P.
99US-0132486P.
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99US-0134370P.
99US-0134768P.
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9905-0135124P-
9905-0135629P-
9905-0136021P-
9905-013632P-
9905-013722P-
9905-013722P-
9905-013722P-
9905-013722P-
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99US-0134256P.
99US-0134218P.
99US-0134219P.
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99US-0138840P.
99US-0138847P.
99US-0139119P.
71.4%;
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                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                5; Conservative
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                               305 LMVVAEF 311
                                                                                                                                                                                                                                                                                                                               termination sequence
 Best Local Similarity
                                               1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2.
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21-APR-1999;
23-APR-1999;
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16-APR-1999;
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                                                                                                                                                                                               AAG20944;
                Matches
                                                                                                                               RESULT 44
                                                                                                                                                  AAG20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system, such as and central nervous systems, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic utilisation of the activities such as: Immune system suppression, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, cancer disgnosis and therapy, drug screening, and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAIS7798-AAI61369) and the
                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, Wang D;
Zhang J, Zhao
                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's Parkinson's disease; hamenstatic; amyotrophic lateral sclerosis; Shy-Brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 4; Length 373;
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Yang Y,
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Xue AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                             AAM40200 standard; protein; 373 AA
                                                                                                                                                                                                          Human polypeptide SEQ ID NO 3345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00552317.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00650312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00727344
                                                                                                                                                                             (first entry)
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                || |||:
VMEVAEY 35
VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                          WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                          leukaemia.
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Wang J, 1
Zhou P, 0
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Score 24; DB 3; Length 378;
Pred. No. 9e+02;
1; Mismatches 1; Indels
9908-0148341P

9908-01488565P

9908-0149368P

9908-0149175P

9908-0149722P

9908-0149722P

9908-0149722P

9908-0149722P

9908-0149930P

9908-0149930P

9908-0151066F

9908-0151066F

9908-0151068P

9908-0151080P

9908-015928P

9908-015928P

9908-015928P

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9908-015928P

9908-016098P

9908-0161359P

9908-0161359P
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5; Conservative
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VMNMAEF
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  12-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
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27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
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Best Local S
Matches 5
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99US-0139452P.
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20 - 7
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9905-0139462P

9905-0139461P

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9905-0140313P

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9905-0140313P

9905-0140313P

9905-0140313P

9905-0144313P

9905-014508P

9905-014508P

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                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 28135.
                       AAG24457 standard; protein; 378 AA
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                                                       (first entry)
                                                                                                                        Arabidopsis thaliana
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05-MAR-1999;

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18-JUN-1999;
18-JUN-1999;
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                                        AAG24457;
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Page 30

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000

Arabidopsis thaliana protein fragment SEQ ID NO: 57657.

18-OCT-2000 (first entry)

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99US-0149723P.
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99US-0149930P.
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99US-0151066F.
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Pred. No. 9e+02;
1; Mismatches 1; Indels
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ilarity 71.4%;
Conservative
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wes 5; Conserv
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VMNMAEF
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AAG45882
ID AAG451
XX
AC AAG451
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Matches
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22-JUL-1999;
22-JUL-1999;
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Human, membrane transport protein, MTRP-1, antiinflammatory, cytostatic, antithyroid, immunosuppressive, thyromimetic, antidiabetic, nootropic, antidiarrheic, neuroprotective, antidepressant, nephrotropic, virucide;
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Pred. No. 9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human membrane transport protein, MTRP-1.
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9905-0151066P

9905-0151030P

9905-0151303P

9905-0151330P

9905-0153070P

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9905-015953P

9905-01603P

9905-01603P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 71.4%;
5; Conservative
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VMNMAEF
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30-AUG-1999;
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Matches
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ID AAX7
AC AAY7
XX AAY 29-P
XX XY Hume
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XX AHUME
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diagnosis, prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzheimer's disease; Apression; schizophrenia; immune disorder; allergy; inflammatory disorder; ADDS; Addison's disease; atherosclerosis; gout; Graves disease; Hashimoto's thyroiditis; microbial infection; cancer; cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                           /note= "P-type cation transporter signature sequence"
antihelminthic; protozoacide; antibacterial; neuroleptic; antigout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guegler KJ;
                                                                                                                                                                       85. .115
/note= "El-E2 ATPase signature sequence"
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/note= "El-E2 ATPase signature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corley NC,
                                                                                                                                    'note= "Phosphorylation site"
                                                                                                                                                          'note= "Phosphorylation site"
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| Jabel = Transmembrane_domain
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/label= Transmembrane_domain
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                                                                                                              Location/Qualifiers
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98US-0172214P.
99US-0121896P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365576/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD00600
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22-DEC-1998;
26-FEB-1999;
                                                                                          Homo sapiens
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                                                                                                                                                                       Region
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Claim 1; Page 89-90; 136pp; English.

The present sequence is a membrane transport protein, MTRP-1 from Incyte clone 961344 isolated from human BRSTTUT03 cDNA library. MTRP-1 shows homology to the mouse BI-E2 ATPase and is expressed in reproductive, nervous and haematopoietic/immune tissues. The present sequence is useful in diagnosis, prevention and treatment of disorders related with increased or decreased expression of MTRP such as familial goitre, Menkes disease, diabetes, Parkinson's disease, neurological disorders such as Alzheimer's disease, depression, epilepsy, schizophrenia, immune/inflammatory disorders such as AlDS, Addison's disease, allergies, atherosclerosis, Graves disease, gout, Hashimoto's thyroiditis, viral,

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bacterial, fungal, parasitic, protozoal or helminthic infections and cell proliferative disorders such as cancer. Fragments of MTRP polymucleotides are useful as targets in microarrays. MTRP DNA is useful for generating hybridisation probes useful in mapping genomic sequences and detecting differences in sequences among normal, carrier and affected individuals. It is also used for screening libraries of compounds in drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM3213) with noorropic, fimunosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
, Zhao Q
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                          Gaps
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Zhang J,
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                                                                                                                                            Score 24; DB 3; Length 384; Pred. No. 9.1e+02;
                                                                                                                                                                         1; Indels
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Yang Y,
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                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as central nervous system injuries.
                                                                                                                                                                                                                                                                                                     AAM40198 standard; protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 3343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US - 00471275.
2000US - 00582317.
2000US - 00552317.
2000US - 00620312.
2000US - 0062450.
2000US - 0063450.
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lang Z, Wehrman T,
                                                                                                                                            82.8%;
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                               305 LMVVAEF 311
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                                                                                                                                                                                                   1 VMXVAEF 7
                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                  Sequence 384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI59354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-2000;
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29-NOV-2000;
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25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                       techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
Wang J,
                                                                                                                                                                                                                                                                                                                                 AAM40198;
                                                                                                                                              Query Match
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                                                                                                                                                                         Matches
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AAM40198
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immunosuppressant and cytostatic activity. The polynucleotides are useful
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                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                  1 VMXVAEF
                                                                                                                                                   Sequence 384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200268593-A2.
                                                                                                                                                                                              'n.
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                                                                                                                                                                                                                                                                                                                 AAE30494;
                                                                                                                                                                                                                                                                                                                                                                                          Gr64A3.
                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                        RESULT 50
                                                                                                                                                                                                                                                                                   AAE30494
  $$$$$$$$$$$$$$$$$$
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Zhao QA;
          localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Humenostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                             Gaps
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Zhang J,
                                                                                                                                                             ö
                                                                                                                                      Score 24; DB 4; Length 384; Pred. No. 9.1e+02;
                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; SEQ ID NO 3344; 10078pp; English.
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R,
Xu C,
                                                                                                                                                                                                                                                            AAM40199 standard; protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Z, Wehrman T, Xu (
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 3344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-0062312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
                                                                                                                                       82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2000; 2000US-00727344
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                 Local Similarity 71.4
                                                                                                                                                                                                      305 LMVVAEF 311
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                                                                                                                                                                                  1 VMXVAEF 7
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                   Sequence 384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153312-A1
                                                                                                                                                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia.
                                                                                                                                                                                                                                                                                 AAM40199;
                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J,
Zhou P,
                                                                                                                                                             Matches
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in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous thy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral seclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid encoding an insect gustatory receptor (Gr) or odorant receptor (Or) protein which comprises seven transmembrane domains and a C-terminal domain comprising consecutive amino acids. The invention is useful for identifying a compound which activates the insect receptor or inhibits the activity of the insect receptor or inhibits the activity of a lipid bilayer. The purified insect receptor protein is embedded in a lipid bilayer. The invention is sprayed for combating ingestion of crops by pest insects, combating disease-carrying insects in an area and controlling a pest population in an area. The invention is useful for detecting the presence of insect gustatory or odorant receptor and for inhibiting the function of the receptor in humans or animals or in biological fluids isolated from them. The invention is also useful for identifying or isolating other insect receptors and for combating pest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding insect gustatory or odorant receptor protein useful for identifying a compound which specifically binds to the receptor for controlling a pest population in an area.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 384;
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Pred. No. 9.18+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fruit fly gustatory receptor protein, Gr64A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 164-166; 264pp; English.
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ilarity 71.4%;
Conservative
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9905-0137724P.
9905-0138094P.
9905-01380447P.
9905-0139452P.
9905-0139452P.
9905-0139452P.
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9905-0139453P.
9905-0140334P.
9905-0140334P.
9905-0140334P.
9905-014033P.
9905-0144085P.
9905-0144085P.
9905-014433P.
9905-01453P.
04-70N-1999;
08-70N-1999;
10-70N-1999;
10-70N-1999;
14-70N-1999;
16-70N-1999;
16-70N-1999;
18-70N-1999;
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23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
29-JUN-1999;
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                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                      Gaps
nuisances. The present sequence is fruit fly gustatory receptor (Gr)
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                                      Length 409;
                                                      1; Indels
                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 57656.
                                     Query Match 82.8%; Score 24; DB 5; L
Best Local Similarity 71.4%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 1;
                                                                                                                         AAG45881 standard; protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                   9905-0139845P
9905-0130077P
9905-0130049P
9905-0131449P
9905-0132448P
9905-0132448P
9905-013248F
9905-013248F
9905-013248F
9905-013248F
9905-013248F
9905-013248F
9905-0134218P
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99US-0123180P.
99US-012548P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
99US-0126785P.
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                                                                                                                                                        18-OCT-2000 (first entry)
                                                                                                                                                                                                                    Arabidopsis thaliana
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24 VLLVAEF 30
                                                                    VMXVAEF 7
                       Sequence 409 AA
                                                                                                                                                                                                                                                                               25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
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14-MAY-1999;
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        protein
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5; Conservative
                                     84 VMNMAEF
                   1 VMXVAEF
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23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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29-MAR-1999;
01-APR-1999;
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16-APR-1999;
19-APR-1999;
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06-MAY-1999;
06-MAY-1999;
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03-JUN-1999;
04-JUN-1999;
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27-MAY-1999;
28-MAY-1999;
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14-MAY-1999;
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24-MAY-1999
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                                                                                                  AAG24456;
  Matches
                                                               RESULT 52
                                 셤
                    8
         9905-0147416P

9905-0147431P

9905-014831P

9905-014831P

9905-014831P

9905-0148341P

9905-0148341P

9905-0149328P

9905-0149426P

9905-0150684P

9905-0151080P

9905-0151080P

9905-0151080P

9905-0151080P

9905-0151080P

9905-015139P

9905-0154039P

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9905-016961P

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9905-0160960P

9905-0160980P

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9905-0160980P

9905-0161361P

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9905-0161361P

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9905-0161361P
06-AUG-1999,
06-AUG-1999,
10-AUG-1999,
11-AUG-1999,
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11-AUG-1999,
11-AUG-1999,
11-AUG-1999,
11-AUG-1999,
12-AUG-1999,
20-AUG-1999,
20-SEP-1999,
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22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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28-SEP-1999;
29-SEP-1999;
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82.8%; Score 24; DB 3; Length 414; 71.4%; Pred. No. 9.9e+02;

Query Match Best Local Similarity

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                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
Gaps
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Indels
                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 28134.
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Mismatches
                                                              AAG24456 standard; protein; 414 AA.
1,
                                                                                                                                                                                                        99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-012664P.
99US-0126764P.
99US-01267462P.
99US-0126734P.
99US-0128234P.
99US-0130891P.
99US-0130891P.
99US-0130891P.
99US-0131449P.
99US-0132484P.
99US-0132487P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
99US-0134234P.
                                                                                                                                                                                            25-FEB-2000; 2000EP-00301439
                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                     termination sequence
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14-JUN-1999;
16-JUN-1999;
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9905-0148655P

9905-0148684P

9905-0149175P

9905-0149172P

9905-0149172P

9905-014910P

9905-0149910P

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9905-0149910P

9905-0150884P

9905-0151800P

9905-0151800P

9905-015180P

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Similarity 71.4%;
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VMNMAEF
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9900S-0144612P

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9900S-0144612P

9900S-0144612P

9900S-0144613P

9900S-014518P

9900S-0147302P

9900S-0147332P
16 - JUN - 1999 | 18 - JUN - 1999 | 19 - JUN - 1
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ö Gaps ö Length 414; Score 24; DB 3; Le: Pred. No. 9.9e+02; 1; Mismatches 1;

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990S-0139459P

990S-0139461P

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990S-0139461P

990S-0139461P

990S-0140823P

990S-0140823P

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990S-0140823P

990S-0140823P

990S-0141234P

990S-014234P

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 18 - 70N - 1999;
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05-AUG-1999

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09-AUG-1999

11-AUG-1999

11-AU
     signal transduction pathway; metabolic pathway; netic mapping; gene expression control; promoter;
                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 23319.
                                      AAG20943 standard; protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           9905-0123180P-
9905-0125788P-
9905-0125788P-
9905-0126785P-
9905-0126785P-
9905-0128714P-
9905-0128714P-
9905-0138714P-
9905-0130449P-
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9905-0130449P-
9905-0131449P-
9905-0131449P-
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9905-0132487P-
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99US-0139457P.
99US-0139458P.
                                                                                                                                                                                  Protein identification, signa hybridisation assay; genetic termination sequence.
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99US-0139452P
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                                                                                                           (first entry)
                                                                                                                                                                                                                                                          Arabidopsis thaliana
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16 - JUN - 1999)
17 - JUN - 1999)
18 - JUN - 1999)
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18-JUN-1999;
18-JUN-1999;
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                                                                           AAG20943;
 RESULT 53
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to convacious and the encoded proteins thereof. Specifically, it refers to convacious desired by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as attribodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these concludate expression of the CDNA molecules. As such, these concludate expression of the CDNA molecules are useful in gene therapy for treating osteoporosis, neurological disease, Albahamer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, noctropic, antiparkinsonian, encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listens of the invention but
                                                                                                                                                                                                                                                                                                                                                           New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                              osteoporosis; neurological disease; Alzheimer's disease;
Parkinson's disease; dementia; short memory; cancer;
sense or motor function; emotional reaction; fear response; panic;
osteopathic; neuroprotectieve; nootropic; antiparkinsonian; cytostatic;
           Human protein useful for treating neurological disease Seq 2913.
                                  human; oligo-capping method; diagnostic marker; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 8; Length 457; 71.4%; Pred. No. 1.1e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                    Nishikawa T, Iso
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2913; 2686pp; English.
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                                                                                                                                                                                                                                                           (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                       14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                12-FEB-2004; 2004EP-00003145
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Matches 5; Conservative
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Wakamatsu A, Ishii S,
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389 LMVVAEF 395
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                                                                                                tranquiliser.
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                                                                                                                          Homo sapiens.
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                                                                                             9905-0151303P.
9908-0151438P.
9908-0151930P.
9908-0152363P.
9908-0153070P.
9908-0153078P.
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99US-0159329P.
99US-0159330P.
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9905-0159637P
9905-0159638P
9905-0160741P
9905-0160767P
9905-0160767P
                                              99US-0150884P.
99US-0151065P.
99US-0151066P.
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99US-0157753P.
99US-0157865P.
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99US-0161359P.
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99US-0161993P
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VMNMAEF 90
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Best Local Similarity
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28-8EP-1999
29-8EP-1999
06-0CT-1999
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06-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
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12-0CT-1999
13-0CT-1999
                                 25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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07-SEP-1999;
10-SEP-1999;
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15-SEP-1999;
16-SEP-1999;
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22-001-1999;
25-001-1999;
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26-001-1999;
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28-OCT-1999;
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Isono Y, Sugiyama T, Otsuki T;

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Gaps

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the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid;

(2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene required for that has an activity against a biological pathway required for proliferation or the biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any one of
                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 2e+03;
0; Mismatches 1; Indels
                                                                   ¥,₹
                                                                   Ohlsen |
Forsyth |
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                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 46060; 1766pp; English.
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                                                                   Malone C,
Carr GJ,
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Similarity 83.3%;
5; Conservative C
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                          (ELIT-) ELITRA PHARM INC.
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                                                                      Zamudio C,
Trawick JD,
                                                                                                                                          2003-029926/02
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Best Local Similarity
Matches 5; Conserv
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                                                                   Wang L,
Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF66431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                               thierry JC, Prieur D, Dietrich J, Lecompte O;
Weissenbach J, Saurin W, Heilig R;
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Pred. No. 1.4e+03;
2; Mismatches 1; Indels
                                           Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #3663
Putative P. abyssi queuine tRNA-ribosyltransferase.
                                                                                                                                                                                                                                                                                                                        (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 957-959; 1657pp; French.
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                               Thierry JC,
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nes 4; Conservative
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440 VMAIAEY 446
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                                                                                         Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 584 AA;
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Querellou J,
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25-OCT-2001;
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06-MAR-2002;
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                                                                                                                                     FR2792651-A1
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Trawick JD,
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Wall D,
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                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
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                                                                                                                                                                                               Disclosure; SEQ ID NO 36873; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 4; Length 817; 71.4%; Pred. No. 2.1e+03; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #3671.
                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU18144 standard; protein; 902 AA.
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                                                                                                          Li PWD,
                                       23-MAR-2001; 2001WO-US009231.
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                         23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                         432 VLLVAEF 438
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                                                                                                                             WPI; 2001-656860/75
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                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus anthracis,
                                                                                                                                        N-PSDB; ABL14130
                                                                                                                                                                                                                                                                                                                             Sequence 817 AA;
WO200171042-A2
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                                                                                                                                                                               interactions
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                   27-SEP-2001
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the invention fraidres to an instance and compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

the folls antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

the folls are proportion of the more comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense continued antisense continued to antisense nucleic acid; (1) a nost cell containing the vector; (1) an isolated continued to polypeptide; (2) producing the polypeptide; (6) inhibiting cellular continued for the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for required for that has an activity against a biological pathway continued for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, activity; (1) manufacturing an antibicit; (10) profiling a compound, activity; (11) a culture comprising strains in which the extent compound, activity; (11) a culture comprising strains in which the extent compound, activity; (11) a culture comprising strains in which the compound is conference or collection of an organism. The antisense nucleic acids are useful for cidentifying proteins or screening for homologous nucleic acids required for for ellular proliferation of an organism. The autisense mulled codes are useful for dentifying proteins or screening for homologous nucleic acids required for confidence or or for granism acrossing acids are useful for dentifying proteins or for granism candidate molecules for rational and account and account of an organism.
                                                                                                                                                                                                                                                                      or screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Xu 田;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #28340.
Carr GJ, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 46068; 1766pp; English.
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the 613 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that inhibits proliferation of an cequired for proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which a proliferation required gene or its gene product lies or a gene on which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The attriense mucleic acids required for cellular proliferation of an organism. The attriense uncleic acids required for cellular proliferation of an organism or the candidate molecules for rational additional accidence or cellular proliferation of the condition or an organism. The attriense mucleic acids required for a second or the candidate molecules for rational
                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 70737; 1766pp; English.
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                                                                                                                                                                Carr GJ,
                                                                                                                                                 Malone C,
            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                   2003-029926/02.
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N-PSDB; ACA46683
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               82.8%; Score 24; DB 6; Length 919;
83.3%; Pred. No. 2.3e+03;
iive 0; Mismatches 1; Indels
Query Match
Query Match
Best Local Similarity 83.33,
Bernan 5, Conservative
                                                                    2 MXVAEF 7
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ADN22714 standard; protein; 919 AA.
                            (first entry)
                            02-DEC-2004
              ADN22714;
BXXXXX
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MSVAEF 123

118

RESULT 60

Bacterial polypeptide #5367.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant comprising the recombinant DNA construct and growing a plant second plant with the method of producing a transformed plant to avoid an improved property comprises transformed plant with the tercombinant DNA construct and growing the transformed plant where the compinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plants with the polynucleotide or polypeptide is useful for producing plants with the recombinant DNA construct is useful for producing plants with the recombinant DNA construct is useful for improving plants with the recombinant plant growth respond cold, hear or drought tolerance, tolerance to herbicides, extreme commonic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the properties in trogen or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by production, improved lignin production or improved galactomannan condition, improved lignin production or improved data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specific promoter positioned to provide New recombinant DNA construct comprising a promoter positioned to provice for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct, transformed plant; improved plant property, Goldman BS; Claim 1; SEQ ID NO 5367; 122pp; English. Chen X, Slater SC, 20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P WPI; 2004-061375/06. CAO Y. HINKLE G J. SLATER S C. GOLDMAN B S. Hinkle GJ, US2003233675-A1. CHEN X. 18-DEC-2003 Bacteria. CAOY/) (GOLD/) SLAT/) (HINK/) CHEN/) Cao Y,

ö Gaps ö 82.8%; Score 24; DB 8; Length 919; 71.4%; Pred. No. 2.3e+03; rive 1; Mismatches 1; Indels 5; Conservative Best Local Similarity Matches 5; Conserv Sequence 919 AA; Query Match

RESULT 61 ADB11880 Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.

Staphylococcus epidermidis.

JS6380370-B1.

30-APR-2002

13-AUG-1998; 14-AUG-1997; 08-NOV-1997;

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4831

(first entry)

24-JUL-2002

ABP39986;

ABP39986 standard; protein; 927 AA.

4BP39986

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New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                 Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                  Alloiococcus otitis antigenic protein SEQ ID NO:5180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen protein from the present invention.
                                                                                                                                                                                                                                                                                  Claim 33; SEQ ID NO 5180; 1019pp; English
                                                                                                                                                                                                       Mcmichael JC, Russell DP,
ADB11880 standard; protein; 926 AA
                                                                                                                                             25-NOV-2002; 2002WO-US036123.
                                                                                                                                                             29-NOV-2001; 2001US-0333777P.
                                                                                                                                                                                      (AMHP ) WYETH HOLDINGS CORP.
                                 (first entry)
                                                                                           Alloiococcus otitis.
                                                                                                                                                                                                                        WPI; 2003-505284/47
                                                                                                                                                                                                                                N-PSDB; ADB11883
                                                                                                            WO2003048304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 926 AA;
                                                                                                                                                                                                       Fletcher LD,
                                20-NOV-2003
                                                                                                                            12-JUN-2003
                 ADB11880,
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Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.

(GENO-) GENOME THERAPEUTICS CORP.

Zagursky RJ;

ä

Bush

2002-381255/41. Doucette-Stamm LA,

N-PSDB; ABN92531

97US-0055779P 97US-0064964P

Disclosure; SEQ ID NO 4831; 267pp; English.

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 5; Length 927;
Pred. No. 2.4e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.8
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polymucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I) an isolated polypeptide that is encoded by the polymucleotide (I), its expression vector comprising the novel isolated polymucleotide (I), its complement, despendent variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polypeptide (I); (5) an immunogenic composition comprising the polypeptides of (I) and a carrier; (I) a protein chip comprising in the expression vector; (6) a pharmacoutical composition composition; (9) detecting and/or identifying Alloiococcus of the polypeptides of (I), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (I0) a kit comprising a container; or the antibody of (4); and (11) producing a polypeptide by culturing the containing the novel polymucleotides, its degenerate variant or fragment; or the antibody of (4); and (11) producing a polypeptide by culturing the polypeptides, polypeptides, its degenerate variant or fragment; or the antibody of (4); and (11) producing a polypeptide by culturing the polymucleotides, polypeptides, its degenerate variant or fragment. Contraining the novel polymucleotides, its degenerate variant or fragment. Contraining the pulpage in the culture. (I) can be used in gene therapy. The polymucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis.
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25-NOV-2002; 2002WO-US036123
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18-NOV-2002; 2002US-0426742P.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                       N-PSDB; ADB11881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 938 AA;
                                                                       WO2003048304-A2.
                                                                                                 12-JUN-2003
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TD ADB1
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AC ADB1
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DT 20-N
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                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated mucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid a comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus sucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SQD ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome and/or plasmids of commercial importance; a computer based system for identifying commercial importance; a computer based system for identifying commercial important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment commercially important in ucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcus epidermidis bacterial infection. This is the amino acid sequence of a S. epidermidis protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                   New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
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Pred. No. 2.4e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                              Claim 17; SEQ ID NO 5691; 741pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB11878 standard; protein; 938 AA.
                                                                                             97US-0064964P.
98US-00134001.
99US-00450969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%;
                                                                  01-DEC-2003; 2003US-00724972.
                                                                                                                                                                                                  Bush D;
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                                                                                                                                                     DOUCETTE-STAMM L.
BUSH D.
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Matches 5, Conservative
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             US2004147734-A1.
                                                                                                                                                                                                                                          N-PSDB; ADS02624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
                                                                                              08-NOV-1997;
                                                                                                             13-AUG-1998;
29-NOV-1999;
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                                         29-JUL-2004.
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                                                                                                                                                     (DOUC/)
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Mail diolocecus ociticidis, antigencic procesti, immunogenic; immunisation; magenet terrepay, Gram-positive bacterium, infection.

Majolocecus ociticis.

Mayono1048104-A2.

Mayono10481
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Aminopeptidase H110D helminthic antigen.
                                                                                                              Aminopeptidase; H110D; antigen; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                  (MLCW ) MALLINCKRODT VETERINARY INC. (AGRI-) AGRIC & FOOD RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith TS,
                                                                                                                                                                                                                                                                                                94WO-GB000204.
                                                                                                                                                                                                                                                                                                                                          93GB-00002302
  (revised)
(first entry)
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532 VISVAEF
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                                                                                                                                                                                                                                                                                           04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                          )5-FEB-1993;
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                                                                                                                                                                                                       WO9418320-A1
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25-MAR-2003
25-MAR-1995
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31-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polymucleotide (I) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis ganomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I)
an isolated polypeptide that is encoded by the polymucleotide (I); (2) an expression vector comprising the novel isolated polymucleotide (I); (2) an expression vector of (I); (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I) and a carrier; (7) a protein chip comprising the expression vector; (6) a pharmaceulical composition comprising the carrier; (7) a protein chip comprising the cypression vector; (6) a detecting and/or identifying an array of the polypeptide of (I); their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (I0) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the polypeptide from the culture. (I) can be used in gene therapy. The polymucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials.

The polymucleotides are useful for expressing and detecting Alloiococcus otitidis The present invention.
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                                          Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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83.3%; Pred. No. 2.4e+03;
iive 0; Mismatches 1; Indels
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Alloiococcus otitis antigenic protein SEQ ID NO:5184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; SEQ ID NO 5184; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Russell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR58701 standard; protein; 962 AA.
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18-NOV-2002; 2002US-0426742P
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                                                                                                              Alloiococcus otitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-505284/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADB11879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 940 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSVAEF
                                                                                                                                                        WO2003048304-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Fletcher LD,
                                                                                                                                                                                                    12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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is expressed in COSI or CHO cells. The recombinant antigen is used in a vaccine for the protection of mammals and animals against the parasite H. contortus. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                The Haemonchus contortus enzyme antigen H110D is an aminopeptidase, and
                                                                                                                                                                                                                                                                             Gaps
Expression of parasite gut membrane bound antigen - for protective immunity against parasites esp. Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helminth; aminopeptidase; H11-3; H11-2; H11-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helminth aminopeptidase H110D varient encoded by the H11-3 gene.
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                                                                                                                                                                                                                                  Query Match 82.8%; Score 24; DB 2; Length 962; Best Local Similarity 71.4%; Pred. No. 2.5e+03; Matches 5; Conservative 1; Mismatches 1; Indels
                                                         Disclosure; Page 23-27; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR51280 standard; protein; 972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGRI-) AGRIC & FOOD RES COUNCIL.
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Best Loc Matches

RESULT 66

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AARSB701 ID AAR! XX AC AAR! XX

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Newton SE;

Rolph TP,

N-PSDB; ABQ74274, ABQ74275

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Human; transporter protein; anorectic; antidiabetic; anti-Parkinsonian; nootropic; neuroprotective; hypotensive; antidepressant; neuroleptic; cardiovascular; mimunosuppressive; gene therapy; sugar homeostasis; obesity; diabetes; amorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypertension; autonomic function disorder; schizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; ischaemia repertusion injury; restenosis; hormonal disorder;
                                                                                             New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation in virus or microbe.
                                                                                                                                                                                                      The sequences given in AAR51280-82 represent varients of the helminth aminopeptidase H110D encoed by the genes H11-3, -2 and -1 respectively. H110D is a protein doublet which shows homolgy to a family of integral membrane aminopeptidases. The differences between the coding sequences and the translated products, can be attributed to different mRNAs of the multigene family, and also to different variants of the H110D-encoding sequence being present at different stages of the life cycle, or in strains differing in geographical origin. Antigenic fragments of these aminopeptidases may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. The DNA sequences encoding these proteins may be incorporated into a virus or microbe and used in a similar manner. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
   Oliver JJ, Newton SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%; Score 24; DB 2; Length 972; 71.4%; Pred. No. 2.5e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 67084FL transporter protein SEQ ID NO:23.
Smith TS, - Munn EA, Knox DP,
                                                                                                                                                                      Claim 6; Page 82-84; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP52161 standard; protein; 1084 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic mucocutaneous candidiasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2000; 2000US-0256240P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Query Match
Beet Local Similarity 71.4°,
Beet Local Similarity
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                     WPI; 1993-386574/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 VISVAEF 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
                                                       N-PSDB; AAQ52489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 972 AA;
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 Graham M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP52161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 68
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WPI; 2002-590672/63.

Curtis RAJ;

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The present sequence represents the human 67084FL protein, which is a member of the transporter family. The transporter family proteins (1) of the present invention have anorectic, antidabetic, anti-Parkinsonian, contropic, neuroprotective, hypotensive, antidabetic, anti-Parkinsonian, contropic, neuroprotective, hypotensive, antidabetics and can be used in gene therapy. The human transporter proteins from the present invention are cardiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are casing assays. The polynucleotides encoding (1) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), crossing clinical trials, or pharmacogenetics), as surrogate markers, controling clinical trials, or pharmacogenetics), as surrogate markers, and in methods of treatment (e.g. therapeutic or prophylactic). (1) are useful for treating disorders characterised by insufficient or excessive crossin of $6708, $67102, $44181, $7363, $67046, $67102, $44181, $7363, $67046, $67102, $44181, $7084FL or $67084alt substrates or production of transport 8099, $46455, $54414, $3763, $67076, $67102, $44181, $7084FL or $67084alt inhibitors. Disorders associated with supar homeostasis cuch as obesity, diabetes or anorexia. Disorders associated with supar homeostasis contensis, $67076, $67102, $44181, $67084FL or $67084alt are e.g. CNS disorders (e.g. Parkinson's disease or Alzheimer's disease, autonomic function disorders (e.g. hypertension injury or earticoparacters (e.g. hypertension arge-related disorders), or immune disorders (e.g. hypothyroidism or hyperthyroidism), crestenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), con immune disorders (e.g. hypothyroidism or hyperthyroidism), con immune disorders (e.g. chromic muccoutaneous candidiasis)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; transporter protein; anorectic; antidiabetic; anti-Parkinsonian; nootropic; neuroprotective; hypotensive; antidepressant; neuroleptic; cardiovascular; immunosuppressive; gene therapy; sugar homeostasis; obesity; diabetes; anorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypertension; autonomic function disorder; schizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; ischaemia reperfusion injury; restenosis; hormonal disorder; hypothyroidism; immune disorder;
                                            New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 82.8%; Score 24; DB 5; Length 1084; Local Similarity 71.4%; Pred. No. 2.8e+03; es 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 67084alt related transporter protein SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP52175 standard; protein; 1084 AA.
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                                                                                                                                                                           Claim 13; Fig 32; 364pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1084 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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22-MAY-2002; 2002US-00154419

US2003143675-A1.

31-JUL-2003

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transporter family. The transporter family proteins are members of the present invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, and undention be used in gene therapy. The human transporter proteins from the present invention are designated thuman transporter proteins from the present invention are designated thuman transporter proteins from the present invention are designated to polynucleotides encoding (1) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, or pharmacogenetics), as surrogate markers, and in methods of treatment (e.g. therappeutic or prophylactic). (1) are useful for treating disorders characterised by insufficient or excessive production of 8099, 46455, 54414, 53763, 67076, 67120, 44181, 67084FD or 67084FL or 67084FL inhibitors Disorders associated with 8099 and obesity, diabetes or anprexia Disorders associated with 5414, 53763, 67076, 67102, 44181, 67084FL or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. amnesia or age-related disorders), cardiovascular disorders (e.g. ischaemia reperfusion injury or restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaneous candidiasis). The present sequence represents a human transporter protein related protein from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes human proteins which are members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 334-339; 364pp; English.
17-DEC-2001; 2001WO-US049060
                                                                                                  18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
                                                                  2000US-0256240P
                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590672/63
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                                                                  15-DEC-2000;
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82.8%; Score 24; DB 5; Length 1084; 71.4%; Pred. No. 2.8e+03;
                      1; Indels
                        1; Mismatches
                        5; Conservative
                                                1 VMXVAEF 7
           Local Similarity
Query Match
                         Matches
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ADD37496 standard; protein; 1084 AA. (first entry) Human transporter 67084FL 1016 LMVVAEF 1022 15-JAN-2004 ADD37496; RESULT 70 셤

Human; transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy; diabetes.

Homo sapiens

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The invention relates to an isolated nucleic acid comprising a CDNA is for a human transporter protein, or its complement, a sequence that is 60 % identical to the CDNA, a fragment comprising at least 30 nucleotides of the CDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the CDNA, Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated antibody that specifically binds to the polypeptide, detecting the presence of the polypeptide or nucleic acid in a sample, a kit, identifying a compound that binds to, or that modulates the activity of, the polypeptide, and modulating the activity of, the polypeptide, and modulating the activity of the polypeptide. The polypeptide or nucleic acid is useful for preparing a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, benesity, epilepsy or diabetes. The present sequence represents a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucksmann MA, Meyers RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 73; 663pp; English.
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                                                                                                                                                 2000US-0233790P.
2000US-0238107P.
2000US-0248364P.
2000US-0248878P.
2000US-0256240P.
2000US-0256288P.
2000US-0256288P.
2000US-0258028P.
2001US-0263169P.
2001US-0263169P.
2001US-00958114.
2001US-00958114.
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2001US-00002769.
2001US-00024623.
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                                                                                                                                                                                                                                                                                                                                                                                                                2002US-00055025
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N-PSDB; ADD37495, ADD37497.
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1016 LMVVAEF 1022
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                                                                                                         12-MAY-2000;
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Matches
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ID ADI2
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23-OCT-2002; 25-OCT-2002; 204-NOV-2002; 2
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Ring HZ,
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Elliott V
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Matches
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IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

Emily (ICF) nucleic acids and proteins. The TWIK-7, IC23927,

TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

Emily (ICF) nucleic acids and proteins may be used for preventing,

CHARLES ICF nucleic acids and proteins may be used for preventing,

CHARLES ICF nucleic acids and proteins may be used for preventing,

CHARLES ICF nucleic associated with decreased expression by rectifying

THE ADDITION OF ADDITION OF THE PROTEINS OF THE SEQUENCES MAY BE USED

CHARLES OWN PRODUCTION OF ICF Proteins or to supplement the patients own production of ICF proteins or to supplement the used as antigens in the production of antibodies against ICF proteins and in assays to identify modulators of ICF protein expression and activity. The antigens in the production of antibodies against ICF proteins may also be anti-ICF protein architecting the presence of ICF proteins in seed as diagnostic agents for detecting the presence of ICF proteins in samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disorders, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disozders.
                                                                                                                       Human; 67084FL; ion channel family; ICF; cancer; leukaemia;
Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curtis RAJ, Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 68; 638pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         29-FEB-2000; 2000US-00515520.
29-FEB-2000; 2000US-0185938P.
03-MAR-2000; 2000US-0185938P.
07-APR-2000; 2000US-0195734P.
11-APR-2000; 2000US-0195939P.
26-APR-2000; 2000US-019599P.
19-SEP-2000; 2000US-019599P.
25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0256288P.
15-DEC-2000; 2000US-0256288P.
21-DEC-2000; 2000US-0256288P.
25-APR-2001; 2001US-0093181.28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2002; 2002US-00146733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2001; 2001US-00024623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADI27974, ADI27976.
                                           (first entry)
                                                                                 Human 67084FL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-069000/07
                                                                                                                                                                                                                                                                                 JS2003165891-A1
                                                                                                                                                                                                                                           Homo sapiens
                                           06-MAY-2004
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AD127975;
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Lee SY, Swarnakar A;
r J, Murage J;
Chang H, Chawla NK;
CM, Policky JL;
sequence represents the human 67084FL protein of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive; antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive; gastrointestinal; thyrointestinal; thyrointestinal; the state of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New TRICH polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of TRICH, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crohn's disease; renal disorder; Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic; protozoal; helminthic; cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                     Length 1084;
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Ison CH, Becha SD, Ding L, Warren BA, Lee
VS, Richardson TW, Marquis JP, Ramkumar J,
PB, Yao MG, Lu Y, Gietzen KJ, Yang YG, CP,
Lee S, Yang J, Gandhi AR, Tribouley CM,
                                                                                                                                                                                                                                                                                                                     Score 24; DB 8; I
Pred. No. 2.8e+03;
1; Mismatches 1;
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2002US-0421033P.
2002US-0421349P.
2002US-0423516P.
                                                                                                                                                                                                                                                                                                                     82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1016 LMVVAEF 1022
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Lee EA;
                                                                                                                                                                                                                   Seguence 1084 AA;
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This interior relates to novel numan transporters and ion channel convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention; antiallergic, cerebroprotective, gastrointestinal, hepatotropic, anticonvulsant, antibarchinal, hepatotropic, anticonvulsant, antiparkinsonian, antibacterial, antiparastic, cardiant, cardiavascular, antihacterial, cardiant, cardiavascular, antihacterial, antibacterial, antibacterial, antibacterial, antiparastic, cardiant, cardiavascular, antihacterial, noctropic activity acting as TRICH agonists or antagonists. In addition the disclosed acting as TRICH agonists or antagonists. In addition the disclosed admormal expression or activity of TRICH, such as neurodegenerative diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of TRICH, such as neurodegenerative disorders (for example myotonic dystrophy, catatonia), endocrine disorders (for example myotonic dystrophy, catatonia), endocrine disorders (for example myotonic dystrophy, catatonia), endocrine cample scleroderma, systemic lupus erythematosus, allergies), cardial, fungal, parastic, protozoal, infections (for example viral, bacterial, fungal, parastic, protozoal, helminthic), cardiavascular disorders (for example dodpasture's syndrome), infections (for example viral, bacterial, fungal, parastic, protozoal, helminthic, cardiavascular disorders (for example atherosclerosis), or hepatic diseases (for example compounds that specifically bind to and modulate the activity of TRICH. The nucleotides can be used to create humanised animals or transgenic animals to model human disease. The present sequence is that of a human converse converse or the present sequence is that of a human converse conver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obesity; diabetes; anorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypertension; automomic function disorder; echizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; tashemia repertuation injury; restenosis; hormonal disorder; hypothyroidism; hypethyroidism; immune disorder; chronic mucocutaneous candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, transporter protein, anorectic, antidiabetic; anti-Parkinsonian, nootropic, neuroprotective, hypotensive, antidepressant, neuroleptic, cardiovascular, immunosuppressive, gene therapy; sugar homeostasis;
                     This invention relates to novel human transporters and ion channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 24; DB 8; Length 1084; 71.4%; Pred. No. 2.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1084 AA;
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The present sequence represents the fundable of anti-protein (1) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, cootropic, neuroprotective, hypotensive, antidepressant, neuroleptic, cardiovascular and immunosuppressive, antidepressant, neuroleptic, cardiovascular and immunosuppressive, antidepressant, neuroleptic, cardiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are designated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and 67084alt. The polynucleotides encoding (1) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), cassays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, conditional trials, or pharmacogenetics), as surrogate markers, and in methods of treatment (e.g. therapeutic or prophylactic). (I) are useful for treating disorders characterised by insufficient or excessive production of 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt substrates or production of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt inhibitors. Disorders associated with sugar homeostasis cuch as obesity, diabetes or anorexia, Disorders associated with 54414, 67084FL or 67084alt are e.g. CNS disorders (e.g. phypertension, depression or schizophrenia), or learning or memory disorders (e.g. hypertension, depression or schizophrenia), or learning or cardiovascular disorders (e.g. hypertension, depression or schizophrenia), or learning or cardiovascular disorders (e.g. hypertension, characterial repertension, hymanal disorders (e.g. hypertension, hymanal signates), and hypertension, hymanal signates or production or schizophrenial, hymanal disorders (e.g. hypertension, hymanal disorders (e.g. hypertension), hymanal disorders (e.g. hypertension), hymanal disorders (e.g. hypertension), hymanal disorders (e.g. hypertension), hymanal diso
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                                                                                                                                                                                           New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaneous candidiasis)
                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the human 67084alt protein, which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.8e+03;
1; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                                                   Claim 13; Fig 36; 364pp; English.
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(MILL-) MILLENNIUM PHARM INC.
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Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                          WPI; 2002-590672/63.
N-PSDB; ABQ74276.
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                                                      Curtis RAJ;
                                                                                                                                                                                                                                                                                  disorders.
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transporter and ion channel; TRICH; atherosclerosis; cancer;

Human TRICH-16 protein.

24-MAR-2003

AAE32082;

'note= "Transmembrane domain"

.153

Domain Domain Domain

cocation/Qualifiers

Homo sapiens

Key Domain

gene therapy

Human;

"Transmembrane

note=

"E1-E2 ATPase

'note=

305

'note= 'note=

> Domain Domain Domain Domain Domain

.199

"Transmembrane domain"

"Transmembrane "Transmembrane "Transmembrane "Transmembrane "Transmembrane "Transmembrane

326. .346

.371

351

'note= 'note=

"El-E2 ATPase domain"

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The present invention describes human proteins which are members of the transporter family. The transporter family proteins (I) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, neuroprotective, hypotensive, antidepressant, neuroleptic, cardiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are designated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and 67084aut. The polymucleotides encoding (I) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trails, or pharmacogenetics), as surrogate markers, and in methods of transpentic or prophylactic). (I) are useful for treating disorders characterised by insufficient or excessive production of 8099, 67102, 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 46185, 511clude disorders associated with sugar production of anorexists of a such as a sociated with 8099 and 46181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 67084FL or 67084alt inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obesity, diabetes or anorexia. Disorders associated with 54414, 53763, 67102, 44181, 67084FL or 67084alt are e.g. CNS disorders (e.g. Parkinson's disease or Alzheimer's disease), autonomic function disorders (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. amnesia or age-related disorders), cardiovascular disorders (e.g. ischaemia reperfusion injury or restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaaneous candidiaasis). The present sequence represents a protein given in comparison with a human transporter protein from the
                                                                                                                                                                                                                                                                                                                                    New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 5; Length 1095; 71.4%; Pred. No. 2.8e+03; ive 1; Mismatches 1; Indels
                                                                    /note= "unspecified"
                                        note= "unspecified"
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 35; 364pp; English.
                                                                                                                                                                                    15-DEC-2000; 2000US-0256240P.
18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
                                                                                                                                                          17-DEC-2001; 2001WO-US049060
                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.**,
                                                      Misc-difference 1005
                                                                                                                                                                                                                                                                                                         WPI; 2002-590672/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1095 AA;
                           Misc-difference
                                                                                                  WO200255701-A2
                                                                                                                             18-JUL-2002
                                                                                                                                                                                                                                                                            Curtis RAJ;
                                                                                                                                                                                                                                                                                                                                                                                  disorders
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1015. .1035 /note= "Transmembrane domain"

.1006

/note=

.978

Domain

Domain Domain

.927

900

'note= 'note= 'note= /note= "Transmembrane domain"

WO200283712-A2

Domain

24-OCT-2002

20-APR-2001; 2001US-0285592P. 27-APR-2001; 2001US-0287263P. 04-MAY-2001; 2001US-028666E. 18-MAY-2001; 2001US-0292042P. 25-MAY-2001; 2001US-0293724P.

12-APR-2002; 2002WO-US011760

12-APR-2001;

domain"

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The invention relates to human transporters and ion channels (TRICH) polypeptides and nucleic acid molecules encoding such polypeptides. TRICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human functional transporters and ion channels (TRICH) polypeptides, useful for preparing a composition for diagnosing or treating a disease associated with decreased expression or overexpression of TRICH e.g.
                                                                                                                                                                                          Baughn MR, Elliott VS, Hafalia AJA, Yang J, Walia NK, Ramkumar J; Forseythe IJ, Lu Y, Tang YT, Yue H, Raumann BE, Lal PG, Azimzai Y Lu DAM, Gandhi AR, Thornton M, Nguyen DB, Arvizu CS, Emerling BM; Swarnakar A, Yao MG, Ding L, He A, Griffin JA, Sanjanwala MM; Gietzen KJ, Lee EA, Xu Y, Au-Young JK, Das D, Lee SY, Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 178-181; 204pp; English.
2002US-0351107P
                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-092996/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD49514.
     22-JAN-2002;
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Gaps

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AAE32082 standard; protein; 1095 AA.

RESULT 75 AAE32082 ID AAE320 XX

1016 LMVVAEF 1022

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1 VMXVAEF 7

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The invention relates to an isolated nucleic acid comprising a cDNA encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the cDNA, a fragment comprising at least 30 nucleotides of the cDNA, as sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the cDNA. Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated antibody that specifically binds to the polypeptide, an isolated antibody that specifically binds to the polypeptide, a kit, identifying a compound that binds to, or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide. The nucleic acid is useful for preparing a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence represents a species homologue of a novel human transporter protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, transporter; cytostatic; anorectic; antidiabetic; anticonvulsant;
gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy;
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                      Score 24; DB 7; Length 1095;
Pred. No. 2.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               ADD37499 standard; protein; 1095 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0221769P.
2000US-0233790P.
2000US-0235107P.
2000US-0238336P.
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2000US-0248878P.
2000US-0256240P.
2000US-0256588P.
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2001US-0263169P.
2001US-00858194.
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2001US-00002769.
2001US-00024623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-00895811
2001US-00919781
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2001US-00964295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-00055025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                       Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transporter 67084alt
                                                                                                                                                                                                                                                                                                                                 1016 LMVVAEF 1022
                                                                                                                                                                                                                                                                                                               1 VMXVAEF
                                                                                                                                                                                                                              Sequence 1095 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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05-OCT-2000;
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15-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 77
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       8588888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                ö
  proteins are useful for preparing compositions for diagnosing or treating diseases or conditions associated with decreased expression or overexpression of functional TRICH e.g. atherosclerosis or cancer. The invention is useful in gene therapy. The present sequence is human TRICH
                                                                                                                                                                                                                                                                                                                                                                                 Transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                             Gaps
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                                                                                                               Score 24; DB 6; Length 1095;
Pred. No. 2.8e+03;
                                                                                                                                            1, Indels
                                                                                                                                                                                                                                                                                                                                                        Mouse phopholipid transporting ATPase, AT2B.
                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curtis RAJ, Glucksmann MA, Meyers RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 86; 663pp; English.
                                                                                                                                                                                                                                                                     ADD37509 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000; 20000S-0238336P.
14-NOV-2000; 2000US-0238336P.
15-NOV-2000; 2000US-0248878P.
15-NOV-2000; 2000US-0256240P.
18-DEC-2000; 2000US-025628P.
21-DEC-2000; 2000US-0258028P.
22-JAN-2001; 2001US-0258194.
31-JUL-2001; 2001US-0085811.
31-JUL-2001; 2001US-0095781.
19-SEP-2001; 2001US-00957664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0233790P
2000US-0235107P
2000US-023816F
2000US-0248364P
2000US-0256240P
                                                                                                                82.8%;
71.4%;
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2000US-0215376P.
2000US-0221769P.
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2001US-00024623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-00972724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-00055025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                            5; Conservative
                                                                                                                                                                                                1016 LMVVAEF 1022
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                                                                                                                                                                       1 VMXVAEF 7
                                                                                                                             Best Local Similarity
                                                                                      Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003143675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2000;
19-SEP-2000;
25-SEP-2000;
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14-NOV-2001;
17-DEC-2001;
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                                                                                                                                                                                                                                                                                                ADD37509;
                                                                                                                  Query Match
                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                             Matches
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1016 LMVVAEF 1022
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF
             06-APR-2001;
11-APR-2001;
                                     25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                  Curtis RAJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI27988;
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                                                                                                                                          encoding a human transporter procein, or its complement, a sequence that its 60 % identical to the cDNA, a fragment comprising at least 30 nucleotides of the cDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the cDNA. Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated are persence of the polypeptide or nucleic acid in a sample, a kit, identifying a compound that binds to the polypeptide, a kit, identifying a compound that binds to or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide, and modulating the activity of the polypeptide, and modulating the activity of the reacting poct-1 for defined associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence represents a novel human transporter protein.
                                                         New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 67084alt; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                  invention relates to an isolated nucleic acid comprising a cDNA
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 24; DB 7; Length 1095; 71.4%; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
  Meyers RE;
                                                                                                           Claim 11; SEQ ID NO 76; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI27978 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000US-0195734P.
11-APR-2000; 2000US-019593P.
26-APR-2000; 2000US-0199799P.
19-SEP-2000; 2000US-0233537P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235059P.
15-DEC-2000; 2000US-0256240P.
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2000US-00518866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2002; 2002US-00146733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0256588P
 Curtis RAJ, Glucksmann MA,
                       WPI; 2003-851783/79.
N-PSDB; ADD37498, ADD37500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 71.9
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 67084alt protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           1016 LMVVAEF 1022
                                                                                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                              Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003165891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI27978;
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 78
ADI27978
                                                                                                                                                                                                                                                                                                                                                                              Matches
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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,

CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC Edmily (ICF) mucleic acids and proteins may be used for preventing.

CT WIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC 53763 ICF nucleic acids and proteins may be used for preventing.

CC diagnosing and treating ICF-related diseases. The sequences may be used

CC diagnosing and treating ICF-related diseases. The sequence may be used

CC diagnosing and treating ICF-related with decreased expression by rectifying

CC diagnosing and protein's genome that affect the activity of

CC patients own production of ICF proteins and in

CC patients own production of antibodies against ICF proteins and in

CC anti-ICF protein antibodies, agonists and antaponists may be used to

CC regulate ICF protein antibodies, agonists and activity. The antibodies may also be

CC samples (e.g. by immunosasay) The nucleic acids and proteins may be used

CC samples (e.g. by immunosasay). The nucleic acids and proteins may be used

CC samples (e.g. by immunosasay). The nucleic acids and proteins may be used

CC samples (e.g. by immunosasay). The nucleic acids and proteins may be used

CC samples (e.g. by immunosasay) and evariately of disorders, e.g. cancers

CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple

CC sclerosas, ephlepsy, hepatic disorders and cardiovascular disorders. This

CC sclerosas, ephlepsy, hepatic disorders and cardiovascular disorders. This

CC sclerosas acident for this patent is also available in electronic format

CC from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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71.4%; Pred. No. 2.8e+03;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 71; 638pp; English.
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2001US-00828035.
2001US-00833081.
2001US-00843128.
                                                                                                                                             19-SEP-2001; 2001US-00957683
25-SEP-2001; 2001US-00964252
25-SEP-2001; 2001US-00964256
17-DEC-2001; 2001US-00964256
                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-069000/07.
N-PSDB; ADI27977, ADI27979.
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RESULT 80
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[1647615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
family (ICF) mucleic acids and proteins. The TWIK-6, IC23927,

[2747611, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[275762] ICF nucleic acids and proteins may be used for preventing,
[2762] ICF nucleic acids and proteins may be used for preventing,
[2763] ICF nucleic acids and proteins may be used for preventing,
[2763] ICF nucleic acids and proteins may be used for treat disorders associated with decreased expression by rectifying
[276] The proteins in a patient's genome that affect the accivity of
[277] The proteins by expressing inactive proteins and in assays to identify modulators of ICF proteins expression and activity. The
[277] The protein antibodies against ICF proteins and activity of
[278] antigens in the production of antibodies against ICF proteins and activity. The autibodies may also be
[278] antigens in the production of antibodies and antagonists may be used to
[279] antigens in the production of antibodies against ICF proteins and activity. The autibodies may also be
[27] antigens in the protein expression and activity. The antibodies may also be
[27] assays to identify modulators of ICF protein expression and activity. The autibodies may also be
[27] assays to identify modulators of ICF proteins may be used
[28] cancel semples (e.g. by immunosasay). The nucleic acids and proteins may be used
[28] concers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
[28] colerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
[28] sequence represents a murine protein used in the scope of the invention.
[28] Note: The sequence data for this patent is also available in electronic
[28] format from USPTO at seqdata.uspto.gov/sequence.ttml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, appha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.8%; Score 24; DB 8; Length 1095; 71.4%; Pred. No. 2.8e+03; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curtis RAJ, Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 81; 638pp; English
                                                                                                                                                  03-MAR-2000; 2000US-00518866.
07-APR-2000; 2000US-0195734P.
11-APR-2000; 2000US-0195993P.
26-APR-2000; 2000US-0199799P.
19-SEP-2000; 2000US-0233537P.
25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235018P.
                                                                                                                                                                                                                                                                                                          21-DEC-2000; 2000US-0258028P.
28-FEB-2001; 2001US-00796720.
06-APR-2001; 2001US-00828035.
11-APR-2001; 2001US-00843128.
                                                                                                                                                                                                                                                                           15-DEC-2000; 2000US-0256240P.
                                                                                   2002US-00146733
                                                                                                                                                                                                                                                                                                                                                                                                 2001US-00957683
                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00964252
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-2001; 2001US-00024623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-069000/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1095 AA;
              US2003165891-A1
                                                                                   LS-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2001;
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The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                      transcription regulatory element; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 7; Length 1176; Pred. No. 3.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #13661
                                                                                                                               Klebsiella pneumoniae polypeptide segid 8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 8879; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
ABO62362 standard; protein; 1176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU28134 standard; protein; 1225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                          expression vector;
                                                                                                                                                                                             Klebsiella pneumoniae protein;
                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0117747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%;
71.4%;
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                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                        Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breton GL, Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacter cloacae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 779 VMKVAQF 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-895346/82.
N-PSDB; ACH95913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-1999;
                                                                                                                                                                                                                                                                                   US6610836-B1.
                                                                                    29-JUL-2004
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                                           ABO62362;
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Matches

Local Similarity

1016 LMVVAEF 1022

1 VMXVAEF 7

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Wang L, Wall D,

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The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate transferase, UDP-N-acetylglucosamine enoylpyruvyl transferase). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of staphylococcal genes. The DNA sequence to control the expression of staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host apainst invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                 Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - us
isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knowles DJC, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 2; Length 36; 83.3%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor protein tyrosine kinase (PTK) subtype tyro-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTK; receptor; protein tyrosine kinase; brain tissue.
                       UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hodgson JE, Ku
Rosenberg M,
                                                                                                                                                                                                                                                                                                    /note= "not specified"
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Misc-difference 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 272; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US002318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0011888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burnham MK,
Reichard RW,
                                                                                                                                                                                                  Staphylococcus aureus
                                                                                                                                                   toxic shock syndrome.
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N-PSDB; AAT83751.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                      WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention relates to an increase acts completely any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(i) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confideration or that has an activity against a biological pathway or that has an activity against a biological pathway or the proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the extent compound activity; (11) a culture compound that inhibits the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for collular proliferation to solate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 56058; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
                                                                                            2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                                                                      25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                       21-MAR-2002; 2002WO-US009107
                                                                       2001US-00815242
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                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945 VMEVAQF 951
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                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACA32004
                                                                                              06-SEP-2001;
                                                                       21-MAR-2001;
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Gaps

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AAW27782;

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RESULT 82 AAW27782

Query Match

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This represents a receptor protein tyrosine kinase (PTK) subtype tyro-9.

The invention provides sequences AAV65308 to AAV65313, AAV65315, and
AAV65317 to AAV65319 that encode proteins having a tyrosine kinase domain
and a tissue expression pattern of a receptor PTK subtype selected from
and a tissue expression pattern of a receptor PTK subtype selected from
tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10, tyro-11,
and tyro-12, respectively. The polymaclecides are useful for the
certion of tyrosine kinase domain sequences and detection of tissue
certion patterns of PTK subtypes. The CDNAs can also be injected into
cocytes, the protein expressed, and expression products screened for
using antibodies against tyrosine kinase epitopes. These subtypes
cocytes, the protein expressed, and expression products screened for
using antibodies against tyrosine kinase epitopes. These
certion protocols are used in the diagnosis of diseases associated with
(receptor) PTKS. Recombinant vectors expressing the subtypes can be used
to treat related diseases e.g. tumours, by introduction of the vectors
into skin transplants, then grafting these into the connective tissue of
the dermis, thus specifically targetting tumours as the proteins are
certion the matrix
                       2; Col 51-52; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-401606/38.
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9 VMKIADF 15
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU83035;
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                       Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU83035
  CCCCX SX TTX BX TX BX TX TX BX XX XX XX XX XX XX CCCCCX XX XX BX X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTK; receptor; protein tyrosine kinase; recombinant; grafting; diagnosis; tumour; skin transplant; connective tissue; tyro-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents a novel receptor protein tyrosine kinase (PTK) belypeptide subtype tyro-9. The invention provides polynucleotide sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13. The PTK subtypes are found expressed predominantly in the brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 23; DB 2; Length 54; 57.1%; Pred. No. 2e+02; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor protein tyrosine kinase (PTK) subtype tyro-9.
                                                                                                                                                                                                                                                                      (SALK ) SALK INST BIOLOGICAL STUDIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Col 51-52; 46pp; English
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N-PSDB; AAV65316.
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                                                                                                                                                                                                                                                                                                                   Lai CHC, Lemke GE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54 AA;
                                                                                                                                                                                                      15-MAY-1992;
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                                                                                                                                                         02-JUN-1995;
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                                                               US5811516-A
                                                                                                            22-SEP-1998
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                  Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay;
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79.3%; Score 23; DB 2; Length 54; 57.1%; Pred. No. 2e+02;
                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse receptor protein tyrosine kinase bek.
                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                              ABU83035 standard; protein; 54 AA.
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94US-00237401.
95US-00456647.
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9 VMKIADF
           1 VMXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54 AA;
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02-MAY-1994;
02-JUN-1995;
                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                  22-SEP-1998;
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                                                                                                                                                                                                                                                           16-JAN-2003
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Matches
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    pattern having at least one receptor protein-tyrosine kinase subtype selected from tyro-1, tyro-2, tyro-4, tyro-5, tyro-6, tyro-7, tyro-8, tyro-10, tyro-11 and tyro-12. The protein is useful in assays to screen various compositions which modulate these protein-tyrosine kinase receptors. The presents sequence represents the amino acid sequence of a receptor protein tyrosine kinase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
a tyrosine kinase domain and a tissue expression
                                                                                                                                                                                                                                                                                                                                            Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay;
                                                                                                                                        Gaps
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                                                                                                                Score 23; DB 6; Length 54;
Pred. No. 2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      Rat receptor protein tyrosine kinase tyro-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 12; 49pp; English.
                                                                                                                                                                                                                                                ABU83019 standard; protein; 54 AA
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94US-00237401.
95US-00456647.
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57.1%;
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                                                                                                                             Local Similarity 57.1
hes 4; Conservative
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Best Local Similarity
Matches 4; Conserva
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N-PSDB; ACA69713.
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VMKIADF 15
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                                                                                                                                                              1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                      US2003013848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54 AA;
                                                                                           Sequence 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
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                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
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                                                                                                                                                                                                                                                               Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 6;
Pred. No. 2e+02;
2; Mismatches 1
                                                                                                                                                                                              Receptor protein tyrosine kinase bFGF-R.
ABU83034 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 12; 49pp; English
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94US-00237401.
95US-00456647.
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57.1%;
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                                                                                                                                 (first entry)
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Best Local Similarity
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Gaps

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Composition for the design or screening of a cytoplasmic Tie2 receptor tyrosine kinase domain modulator, comprises a monoclinic or orthorhombic crystalline form of a cytoplasmic Tie2 receptor tyrosine kinase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human Tiez receptor tyrosine kinase domain polypeptide in a monoclinic, or orthorhombic crystalline form. Tiez is an endothelial-specific receptor tyrosine kinase thought to be involved in vascular development. Naturally occuring R849W and Y897S mutations in the Tiez protein have been identified in human s and have been shown to segregate with the autosomal dominant condition vascular dysmorphogenesis. The invention also comprises methods for designing modulators of the biological activity of the cytoplasmic Tiez receptor tyrosine kinase domain is used to design or screen for a modulator of the kinase by rational drug design, using computer models. The present sequence represents residues $59-647, of human fibroblast growth factor receptor I (FGFRI). The catalytic domain of FGFRI closely resembles that of Tie 2 and they share 45 percent sequence identity
               Tie2, Tie2K; human, crystal structure; vascular dysmorphogenesis; protein co-ordinate data; receptor tyrosine kinase; FGFR1; vascular development; fibroblast growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to the 3 dimensional crystal structure of
                                                                                                                                                                                                                                                                                                                                                       Hassell AM, Holmes WD, Shewchuk LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 579; 581pp; English.
                                                                                                                                                                                                                              06-SEP-2001; 2001WO-US027486.
                                                                                                                                                                                                                                                                       08-SEP-2000; 2000US-0231398P.
                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                       Davis RG, Ellis BP,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-292263/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
                                                                                                                                          WO200220734-A2
                                                                                                       Homo sapiens
                                                                                                                                                                                     14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
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Gaps ö 79.3%; Score 23; DB 5; Length 56; 1; Indels Pred. No. 2.1e+02; 2; Mismatches 1; 57.18; Local Similarity 57.1 Les 4; Conservative 1 VMXVAEF 7 Query Match Matches à

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|| :|:| 45 VMKIADF 51

ABP31047 standard; protein; 68 AA. (first entry) 08-JUL-2002 ABP31047; RESULT 8: ABP31047

Human ORF20 protein, SEQ ID NO:40.

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; disbetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary;

Sequences ABP31028-ABP35561 represent 4534 novel human proteins
designated ORF (open reading frame) 1-4534, and sequences ABN75054C designated ORF (open reading frame) 1-4534, and sequences ABN75054ABN79587 represent CDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORFN-ORFW4534 (collectively
CC referred to as ORFX) proteins, polymucleotides at least 85% identical to
the ORFX nucleic carid sequences, vectors and host cells comprising ORFX
CC polypeptides, the recombinant production of ORFX proteins, antibodies
CC splypeptides, methods of screening individuals for a predisposition to an
CORFX-associated disorder. The ORFX proteins of the invention have a wide
CC cativity, and methods of screening individuals for a predisposition to an
CORFX-associated disorder. The ORFX proteins of the invention have a wide
CC call differentiation, immune modulation, hammatopoiesis regulation,
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC chemokinetic activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins
CC chemokinetic activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins
CC cher proliferative disorders such as psoriasis and benign tumours,
CC cher proliferative disorders such as psoriasis and benign tumours,
CC cher proliferative disorders such as epilepsy and Alzheimer's disease,
CC cradiovascular diseases, immune system disorders and disorders such as epilepsy and Alzheimer's disorders and disorders such as epilepsy and alzheimer's disease,
CC cradiovascular diseases, in the detection of ORFX genomic sequences
CC cradiovascular in the identification and cloning of homologous
CC cradiomatorial in the identification and conding of protein, and in drug screening. The ORFX proteins and mortein acids may additionally be used to proceins and acid p neuroprotective, antiatherosclerotic, anticoagulant, thrombolytic, cardiant, hypotensive, antithyroid, antiinflammatory, immunomodulator, dermatological, analgesic, virucide, antibacterial, fungicide. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ diagnosis, treatment and monitoring of ORFX-associated diseases vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; Claim 10; Page 280; 2508pp; English. 24-MAY-2001; 2001WO-US017076. 24-MAY-2000; 2000US-0206690P. Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. 2002-106200/14. N-PSDB; ABN75073 transplantation Sequence 68 AA; WO200190366-A2. Homo sapiens. 29-NOV-2001,

ö Gaps . 79.3%; Score 23; DB 5; Length 68; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 1; Indels 5; Conservative Query Match Best Local Similarity Matches 5; Conserv 2 MXVAEF 1 MLVAEF g ò

ABM37932 standard; protein; 84 AA

ABM37932:

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the creatment, prevention and diagnosis of medical conditions caused by the creatment, prevention and diagnosis of general same associated by the disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting ample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used a antigens in the production of antibodies generally the consequence of presence or acnes indections. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and cativity of P. acnes polypeptides may also be used as
                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 4; Length 84;
Pred. No. 3.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #2309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 2608; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                              AAU41413 standard; protein; 84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS59515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 84 AA;
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                                                                                                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001.
                                                                                                                                                         AAU41413;
RESULT 90
                                 Adua1413

Adua1413

AAUA

AAUA
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The invention relates to an isolated polymuclectide (ACF64435-ACF64733)

cucoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ABM35634-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a colymention; and an isolated T cell population comprising T cells prepared to invention; and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymentials, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the development of P. acnes in compositions, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne polypeptides are useful for diagnosing, preventing or treating acne polypeptides are useful for diagnosing, preventing or treating acne controlly protein. The polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a polypeptide predicted to be encoded by an ORF (open cadding frame) contained within the P. acnes polymention. Sequence against for the printed specification, but was obtained in electronic format directly from without the printed specification, but was obtained in electronic format directly from protein invention. Bequence and the printed specification, but was obtained in electronic format directly from the printed specification, but was obtained in electronic format directly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carter D;
                                                                                                                   Propionibacterium acnes predicted ORF-encoded polypeptide #2608.
                                                                                                                                                                Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing DH, Bhatia A,
Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 2608; 1481pp; English.
                                                                                                                                                                                               immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001US-00978825.
                                                                   (first entry)
                                                                                                                                                                                                                                       Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-381789/36.
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                                                                      20-OCT-2003
                                                                                                                                                                                                                                                                                                                                      24-APR-2003
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Gaps

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DB 6; Length 84; 2; Indels

Score 23; DB 6; I Pred. No. 3.2e+02; 1; Mismatches 2,

h 79.3%; Similarity 57.1%; 4; Conservative

Query Match Best Local Similarity

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Gaps

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4; Conservative

72 VMAIGEF 78

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1 VMXVAEF

Best Loca Matches

ADJ84523

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AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins.

AAB87731 to AAB8784 represent T2R proteins, and AAB87925 to AAB87930 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and genetic modulation of taste signalling pathways.

Modulatory compounds comprising T2R proteins can therefore be used in food and pharmacoulogical industries to customise taste, for e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be used in food and pharmaceutical industries to customize taste, for e.g. to decrease the bitter taste of food.
                                                                                                                                                                                                                                                                        Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor; taste transduction G-protein coupled receptor; identification; tongue; taste sensory neuron; taste cell; taste modulator; food; taste signalling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 4; Length 90; 42.9%; Pred. No. 3.5e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adler JE, Ryba N, Mueller K, Hoon M;
                                                                                                                                                                                                                                      Human T2R22 amino acid sequence SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the bitter taste of food or drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 177; 249pp; English.
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                                                                                                                          AAB87752 standard; protein; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000; 2000WO-US024821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999; 99US-00393634
22-FEB-2000; 2000US-00510332
                                                                                                                                                                                                  (first entry)
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VMAIGEF 78
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VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                  16-MAY-2001
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                                   72
                                                                                                                                                                AAB87752;
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                                                                                                         AAB87752
                                                                                        RESULT
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The invention describes an isolated taste transduction G-protein coupled receptor (1) e.g., T2R which is expressed in a taste cell, comprises greater than 60% sequence identity to a fully defined sequence of 335 (S1), 333 (S2), 299 (S3), 310 (S4), 224 (S5), 77 (S6), 209 (S7), 266 (S16), 165 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S15), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S16), 300 (S10), 160 (S10), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S16), 300 (S10), 160 (S10), 300 (S10), 150 (S11), 170 (S4), 266 (S16), 160 (S16), 160 (S10), 160 (S10), 160 (S10), 160 (S10), 160 (S10), 160 (S11), 170 (S11), 160 (S11), 160 (S11), 160 (S11), 170 (S11), 160 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
                                                                                                                                                                                      taste transduction; G-protein coupled receptor; T2R; taste signaling; CAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoon M, Ryba N, Mueller K;
                                                                                                                                            Human T2R G-protein coupled receptor seg id 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; SEQ ID NO 76; 121pp; English.
ADJ84523 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-2003; 2003US-00364861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00393634
                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-203221/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUKER C S.
ADLER J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RYBA/) RYBA N. (MUEL/) MUELLER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADJ84524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF
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                                                                                                                                                                                                                                                                                                                                US2004038312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1999;
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                             20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2004
                                              ADJ84523;
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Local Similarity 42.9

Matches

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The invention relates to a novel enterohaemorragic Bscherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 057:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                   Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%; Score 23; DB 7; Length 112
71.4%; Pred. No. 4.4e+02;
....matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyperthermophile Methanopyrus kandleri protein #431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 1692; 2067pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM25825 standard; protein; 123 AA.
                                                                                                                                           enterohaemorragic; anti-bacterial
                                                                                                                                                                                                                                                                                                                24-JAN-2002; 2002JP-00015959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-2003; 2003WO-US006664.
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14-MAY-2002; 2002US-0380423P.
16-SEP-2002; 2002US-0410974P.
                                                                                                                                                                                                                                                                                                                                                         24-JAN-2001; 2001JP-00112010
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                                                                                                                                                                                      Escherichia coli; 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4.
Si Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                (UYTS-) UNIV TSUKUBA
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-451640/43.
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66 VMYVAKF 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003076575-A2
                                                                                                                                                                                                                             JP2002355074-A.
                                                            04-DEC-2003
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                   ADC01644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention is related to a novel method of identifying a compound that modulates the activity of a TIR or T2R taste receptor. The method comprises providing a eukaryotic cell that expresses a functional TIR or T2R taste receptor and a G protein that couples to it, contacting the eukaryotic cell with a compound and identifying whether the compound modulates the activity of TIR or T2R expressed by the eukaryotic cell based on its effect on MARK activity, CAMP accumulation or adenylyl cyclase activity. The method is used to identify a compound that blocks or bitter taste associated with a particular T2R activator or that blocks or chances umami taste elicited by a compound that activates the TIRZ/TIR3 (umami) taste receptor or sweet taste elicited by a compound that activates the TIRZ/TIR3 (sweet) taste receptor. The method is useful in activates the TIRZ/TIR3 (sweet) taste elicited by a compound that compound that activates the activity of a TIR or T2R taste receptor. The present sequence is that of a human T2R taste receptor creceptor. The present sequence is that of a human T2R taste receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a compound that modulates the activity of a T1R or T2R taste receptor by assaying the effect of the putative modulatory compound on MAPK activation, cAMP accumulation or adenylyl cyclase activity in the
                                                                                                                                                                                                                                                                                        T2R; taste receptor; G protein; modulatory compound; MAPK activity; accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R22;
                                                                                                                                                                                                                                            Taste receptor modulation-related human T2R22 protein sequence SeqID40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.3%; Score 23; DB 8; Length 90; 42.9%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 40; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu H;
                                                                                                                   ADR29101 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brust P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2003; 2003US-0444172P.
26-MAR-2003; 2003US-0457318P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2004; 2004WO-US002987.
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                        T1R; T2R; taste receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Servant G, Ozeck M,
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ILAIAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-604341/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SENO-) SENOMYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::|||
11 ILAIAEF 17
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                                                                                                                                                                                                                                                                                                                                                                                                               WO2004069191-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eukaryotic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                     04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2004
                 7
                                                                                                                                                            ADR29101;
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ADR29101
DD ADR39101
DD ADR39101
DD ADR39101
DD DE Tas ADR DD DE Tas DD DE T

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Gaps

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(FIDE-) FIDELITY SYSTEMS INC

ADC01644 standard; protein; 112 AA.

RESULT 95 ADC01644 ID ADC01

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Length 112;

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                                                                                                                                                                                                                                                                                                                                                                                                               hyperthermophile Methanopyrus kandleri, the invention also comprises the complete genome from Methanopyrus kandleri. The Methanopyrus kandleri proteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus kandleri genome is useful in a variety of diagnostic and analytical methods. The present amino acid sequence represents a Methanopyrus kandleri protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Enterococcus faecalis polynucleotides and bolypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for
                                                                                                                                                                                                       New isolated nucleic acids encoding any of about 1700 Methanopyrus kandleri proteins, and the encoded proteins, useful as a medicaments or as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid sequence of proteins from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 7; Length 123; 66.7%; Pred. No. 4.9e+02; ive 1; Mismatches 1; Indels
                                                          Pavlova N, Kozyavkin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3642; 193pp; English.
                                                                                                                                                                                                                                                                                                                            Claim 31; SEQ ID NO 431; 1023pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis polypeptide #237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH85757 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00134000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                          Pavlov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis.
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                                                                                                              WPI; 2003-748383/70.
N-PSDB; ADM27081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MXVAEF 7
(MALY/) MALYKH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADH82352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 123 AA;
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MTIAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial
                                                       Slesarev AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6617156-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1997;
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ADH85757
SX CCCCCCX SX FFFFX SX FFF SX FF SX FFF SX FF SX FF SX FFF SX FF SX FFF SX FF SX FFF SX FF SX FF
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This invention describes a novel protein conjugate (I) comprising at least 1 functional region (FR) at any position in the sequence of a carrier protein (II) to form a capaid three-dimensional structure of the Lumazine synthase (LS) type, such that the outer periphery is covalently invention also describes (I) a hetero-oligomeric linked to many FR. The invention also describes (I) a hetero-oligomeric confidence (II) of of at least 1 (I) and at least 1 (II) that lacks FR, with the components optionally covalently linked by chemical treatment; confidence (I) of (I) (4) a DNA (III) that encodes (I); (5) LS from preparation of (I) and (II); that encodes (I); (5) LS from Bacillus subtilis with Cys 33 and/or Cys139 replaced by Ser; (6) DNA (III) encoding LS from Aquifex acolius which is codon-optimized for expression in a recombinant Escherichia coli strain; (7) a chimeric protein (CP) comprising amino acids (aa) 1-60 from is of B. subtilis and a fl.154 from LS of A. acolius for use as (II); and (8) pharmaceutical compositions and vaccines containing (I) and (Ia). The products of the invention have cycostatic, antivixal and antibacterial activity and can be used in a vaccine or for gene therapy. (I) are used as pharmaceuticals
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producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lumazine synthase; capsid; cytostatic; antiviral; antibacterial; vaccine; gene therapy; immunotherapy; biosensor; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein conjugate based on lumazine synthase as carrier, useful e.g. for vaccination and immunotherapy, contains many functional molecules attached to outside of the carrier.
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                            Length 132;
                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeoglobus fulgidus lumazine synthase protein.
                                                                                                                                                                                                                          79.3%; Score 23; DB 7; I
57.1%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB10816 standard; protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8; 180pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fischer M, Bacher A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-572230/53.
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACH/) BACHER A.
                                                                                                                                                                                                                                                                                                                    1 VMXVAEF
                                                                                                                                                                                   Sequence 132 AA;
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                                                                                                                                                                                                                               Query Match
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AAB10816
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              tumors) and in vaccines, including multivalent vaccines, against bacterial or viral infections, to produce diagnostic or therapeutic antibodies, for selections, to produce diagnostic or therapeutic antibodies, and for preparation of protein libraries. (I) may also be used as blosensors and for diagnosis, e.g. of tumors Genes that encode (I) are useful in DNA vaccines and for preparation of plant-based oral vaccines. (I) can contain many FR (same or different) at the surface of a spherical particle (LS comprises 60 subunits that assemble into an icosahedron). The large number of FR may increase sensitivity in immunoassays and the efficiency of immunotherapy agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Bseudomonas aeruginosa and Enterococcus facalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify
 for immunotherapy of human immune deficiency virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr GJ;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prokaryotic cellular proliferation protein; antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                             79.3%; Score 23; DB 3; Length 143; 83.3%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis cellular proliferation protein #39.
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                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU33403 standard; protein; 150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-0207727P
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0254625P.
22-DBC-2000; 2000US-0259318P.
16-PEB-2001; 2001US-0269308P.
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2000US-0206848P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                       Query Match
Best Local Similarity
The 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                 MVVAEF 13
                                                                                                                                                                                                                                                                                                              2 MXVAEF 7
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                                                                                                                                                                                                           Sequence 143 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000;
23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense;
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AAU33403
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            antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antiense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
to express these proteins, and to obtain
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Pred. No. 6e+02;
2; Mismatches
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-439-992A-2 US-08-323-430-12 US-08-252-991A-32931 US-09-162-809-8 US-09-091-219-25 US-09-091-219-25 US-09-091-219-2 US-09-551-25 US-09-551-25 US-09-551-25 US-09-235-451-19 Sequence US-09-235-451-19 Sequence US-09-235-451-19 Sequence	US-09-134-001C-4003 Sequence US-09-489-019A-12512 Sequence US-09-248-796A-16707 Sequence US-07-741-940-6 Sequence US-08-289-548A-6 Sequence US-08-452-654-6 Sequence US-08-452-658-6 Sequence US-08-65-336-3 Sequence US-08-865-336-3 Sequence	US-08-450-582-6 Sequence US-08-449-731-6 Sequence US-00-741-940-4 Sequence US-08-289-548A-4 Sequence US-08-452-6558-4 Sequence US-08-452-6558-4 Sequence US-08-450-582-4 Sequence US-08-449-731-4 Sequence US-09-949-016-10154 Sequence US-09-949-016-10154 Sequence US-09-949-016-10154 Sequence	US-09-073-024 US-09-543-681A-5983 US-09-543-681A-5983 US-09-107-532A-4840 US-09-107-532A-4840 US-09-583-110-4402 US-09-107-433-46600 US-09-110-4402 US-09-131-10-4402 US-09-134-001C-4160 US-09-134-001C-4160 US-09-252-991A-28986 US-09-252-991A-28986 US-09-134-001C-4160 US-09-134-001C-4160 US-09-134-001C-4160 US-09-134-001C-4160 US-09-134-001C-4160 US-09-134-001C-4165 US-09-134-001C-4165 US-09-134-001C-5162 US-09-134-001C-516	2 US-08-702-367A-11 Sequence 11, Appl 15 PCT-0895-046811-11 Sequence 11, Appl 16 US-08-162-046811-11 Sequence 11, Appl 2 US-08-673-789-6 Sequence 10, Appl 17 US-08-162-089-10 Sequence 10, Appl 18 US-08-162-089-14 Sequence 11, Appl 2 US-08-368-776A-11 Sequence 11, Appl 3 US-08-368-776A-12 Sequence 11, Appl 2 US-08-42-635-2 Sequence 12, Appl 18 US-08-162-089-18 Sequence 17, Appl 2 US-08-449-645A-17 Sequence 17, Appl 2 US-08-368-776A-2 Sequence 17, Appl 3 US-08-368-776A-2 Sequence 17, Appl 3 US-08-368-776A-2 Sequence 17, Appl 5 PCT-US95-04681-17 Sequence 17, Appl 5 PCT-US95-04681-17 Sequence 21, Appl 5 PCT-US95-04681-17 Sequence 21, Appl 5 PCT-US95-04681-17 Sequence 216, Appl 4 US-09-536-784-216 Sequence 216, Appl 5 US-08-536-784-216 Sequence 216, Appl 6 US-08-536-784-216 Sequence 216, Appl 7 US-08-132-13-34771, Appl 7 US-09-107-17-17-17-17-17-17-17-17-17-17-17-17-17
3 US-08-439-992A-2 3 US-08-323-430-12 4 US-09-252-991A-32931 5 US-08-162-809-8 3 US-09-091-219-25 5 US-09-091-219-25 6 US-09-60-541-25 6 US-09-60-541-25 7 US-09-60-541-2 8 US-09-60-541-2 8 US-09-60-541-2 8 US-09-578-303-19 8 Equence	3 US-09-134-001C-4003 Sequence 4 US-09-489-039A-12512 Sequence 4 US-09-248-796A.16707 Sequence 1 US-07-741-940-6 Sequence 1 US-08-289-548A-6 Sequence 1 US-08-452-654-6 Sequence 1 US-08-452-655B-6 Sequence 2 US-08-865-336-4 Sequence 2 US-08-865-336-4 Sequence	3 US-08-450-582-6 Sequence 4 US-08-449-731-6 Sequence 1 US-00-741-940-4 Sequence 1 US-08-459-548A-4 Sequence 1 US-08-452-6558-4 Sequence 1 US-08-452-6558-4 Sequence 2 US-08-450-582-4 Sequence 4 US-08-450-582-4 Sequence 4 US-08-450-582-4 Sequence 5 US-09-949-016-10154 Sequence 6 US-09-949-016-10154 Sequence 7 US-09-605-858-34	4 US-09-073-030-224 4 US-09-543-681A-5983 5 Sequence 4 US-09-202-540-13539 5 Sequence 4 US-09-107-532A-4840 5 Sequence 4 US-09-583-110-4402 5 Sequence 4 US-09-1107-433-4600 5 Sequence 4 US-09-489-039A-13610 5 Sequence 5 US-09-489-039A-13610 5 Sequence 6 US-09-134-001C-4160 7 US-09-134-001C-4160 7 US-09-134-001C-4160 7 US-09-134-001C-5362 7 US-09-134-001C-4425 7 US-09-134-001C-5362 7 US-09-134-	US-08-702-367A-11 Sequence PCT-U895-04681-11 Sequence US-08-162-809-10 Sequence US-08-673-789-6 Sequence US-09-949-016-6502 Sequence US-08-162-809-14 Sequence US-08-162-809-14 Sequence US-08-162-809-18 Sequence US-08-162-809-18 Sequence US-08-162-809-18 Sequence US-08-162-809-18 Sequence US-08-162-809-18 Sequence US-08-162-809-18 Sequence US-09-949-016-6501 Sequence US-09-949-016-6501 Sequence US-09-949-016-6501 Sequence US-09-949-016-809-12 Sequence US-09-949-016-809-12 Sequence US-09-136-784-216 Sequence US-09-136-784-216 Sequence US-09-136-784-216 Sequence US-09-128-352-5138 Sequence US-09-28-310-5274 Sequence US-09-28-310-5274
79.3 822 3 US-08-439-992A-2 Sequence 79.3 822 3 US-08-323-430-12 Sequence 79.3 954 4 US-09-252-991A-3291 Sequence 79.3 2232 4 US-09-091-219-25 Sequence 79.3 2232 4 US-09-091-219-25 Sequence 79.3 2232 4 US-09-660-541-25 Sequence 79.3 2247 3 US-09-660-541-2 Sequence 79.3 2247 4 US-09-660-541-2 Sequence 79.3 2247 4 US-09-660-541-2 Sequence 75.9 61 4 US-09-235-451-19 Sequence 75.9 61 4 US-09-378-303-19 Sequence 75.9	75.9 67 3 US-09-134-001C-4003 Sequence 75.9 116 4 US-09-489-038A-15712 Sequence 75.9 116 4 US-09-489-038A-16707 Sequence 75.9 185 1 US-09-248-7548A-6 Sequence 75.9 185 1 US-08-254-548A-6 Sequence 75.9 185 1 US-08-452-658-6 Sequence 75.9 185 1 US-08-453-638-6 Sequence 75.9 185 2 US-08-86-333-3 Sequence 75.9 185 2 US-08-86-333-3	75.9 185 3 US-08-450-582-6 Sequence 75.9 185 4 US-08-4450-731-6 Sequence 75.9 210 1 US-08-248A-4 Sequence 75.9 210 1 US-08-289-548A-4 Sequence 75.9 210 1 US-08-452-654-4 Sequence 75.9 210 1 US-08-452-658-4 Sequence 75.9 210 4 US-08-450-582-4 Sequence 75.9 210 4 US-08-449-731-4 Sequence 75.9 221 4 US-08-449-731-4 Sequence 75.9 221 4 US-08-449-731-4 Sequence 75.9 221 4 US-08-949-016-10154 Sequence 75.9 221 4 US-08-588-34 Sequence 75.9 251 3 US-08-588-34 Sequence	75.9 275 4 US-09-079-030-224 75.9 320 4 US-09-543-681A-5983 Sequence 75.9 379 4 US-09-107-532A-4840 Sequence 75.9 392 4 US-09-107-532A-4840 Sequence 75.9 397 4 US-09-107-532A-4840 Sequence 75.9 400 4 US-09-107-433-4600 Sequence 75.9 447 4 US-09-110-440 Sequence 75.9 445 4 US-09-489-03A-13610 Sequence 75.9 463 3 US-09-134-001C-4160 Sequence 75.9 463 4 US-09-134-001C-4160 Sequence 75.9 497 4 US-09-134-001C-4160 Sequence 75.9 497 4 US-09-134-001C-4160 Sequence 75.9 605 2 US-09-134-001C-5362 Sequence 75.9 605 2 US-09-134-001C-5362 Sequence 75.9 605 2 US-09-134-001C-4425 Sequence 75.9 605 2 US-09-134-001C-4425 Sequence 75.9 605 2 US-09-134-001C-4125 Sequence 75.9 970 2 US-08-449-645A-11 Sequence	2 US-08-702-367A-11 Sequence 5 PCT-US95-04681-11 Sequence 1 US-08-162-809-10 Sequence 2 US-08-673-789-6 Sequence 4 US-09-949-016-6502 Sequence 3 US-08-162-809-14 Sequence 3 US-08-162-809-14 Sequence 3 US-08-162-809-18 Sequence 1 US-08-162-809-18 Sequence 2 US-08-162-809-18 Sequence 2 US-08-162-809-18 Sequence 2 US-08-162-809-18 Sequence 2 US-08-445-417 Sequence 3 US-08-465-117 Sequence 4 US-09-949-016-6501 Sequence 5 PCT-US95-04681-17 Sequence 4 US-09-949-016-6501 Sequence 5 PCT-US95-04681-17 Sequence 6 US-08-961-083-216 Sequence 6 US-08-961-083-216 Sequence 6 US-08-961-083-216 Sequence 6 US-08-961-083-216 Sequence 6 US-09-356-784-216 Sequence 6 US-09-358-784-216 Sequence 6 US-09-328-352-5138 Sequence 6 US-09-283-110-5274 Sequence 7 US-09-283-110-5274 Sequence

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guitabal
APPLICANT: Basi, Minh Tam
APPLICANT: Power, Michael
APPLICANT: Figon, No. 6830918mand
APPLICANT: Frigon, No. 6830918mand
APPLICANT: Frigon, No. 6830918mand
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Hang, Jay
APPLICANT: Hang, Jay
APPLICANT: Blan Pharmaceuticale, Inc.
APPLICANT: Blan P
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OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: inhibitor P3-P4' XD-V
PEATURE:
                          APPLICANT: McConloque, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 28 - 405.NEWC2
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR PILING DATE: 2000-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.1%; Score 27; DB 4; Length 7; 100.0%; Pred. No. 4.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
    APPLICANT: Wang, Shuwen
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NAME/KEY: MOD_RES
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15092, A
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6988, Ap
11165, A
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                                   US-09-915-182-2
US-09-591-279A-45
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US-09-543-681A-5423
US-09-489-019A-9163
US-09-489-019A-11123
US-09-538-092-851
US-09-538-092-1047
US-09-538-092-1047
US-09-548-10653
US-09-248-766A-19658
US-09-248-776A-19658
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PCT-US96-08899-2
US-09-538-0959-383
US-09-949-016-8572
US-09-258-991A-22095
US-09-538-092-1357
US-09-252-991A-27932
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US-09-913-301-2
US-09-902-540-10725
US-09-252-991A-24682
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US-09-252-991A-33109
US-09-949-016-6988
US-09-949-016-11165
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US-09-949-016-10902
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US-08-924-376-2
US-08-685-212-2
US-09-173-151A-31
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US-08-406-824A-6
US-09-949-016-6000
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US-08-702-367A-19
PCT-US95-04681-19
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US-09-908-855-15
US-07-821-716-2
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US-09-724-566A-78
Sequence 76627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Prigon, No. 6627739mand
APPLICANT: Prigon, No. 6627739mand
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
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 $\begin{array}{c} 7.75 \\ 7.$

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0; Gaps
                                                                 APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270-006430US
CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR PILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/139,172
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 81
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Regents of the University of California
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
VENTION: SF, a No. 6558910el Family of Taste Receptors
NNCE: 02307E-098000US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.1%; Score 27; DB 4; Length 8; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Xaa is hydroxyethylene or statine. US-09-471-669A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITE OF INVENTION: SF, a NO. 6558910el Fant; FILE REFERENCE: 02307E-098000US; CURRENT APPLICATION NUMBER: US/09/393,634; CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80, Application US/09393634
Patent No. 6558910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Biliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: human GR24
US-09-393-634-80
Power, Michael
Sinha, Sukanto
Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
7; Conservative
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NAME/KEY: MOD_RES
LOCATION: (4)
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US-09-393-634-80
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APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
CURRENT APPLICATION NUMBER: US,09/724,566A
CURRENT APPLICATION NUMBER: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.1%; Score 27; DB 4; Length 8; 100.0%; Pred. No. 4.1e+05; rive 0; Mismatches 0; Indels
                                                                                                                                             0; Indels
                                                                                            93.1%; Score 27; DB 4; Length 7; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
LOCATION: (3) 7. OTHER INFORMATION: Xaa is hydroxyethylene or statine US-09-471-669A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAWE/KEY: MOD_RES
1 LOCATION: 4
1 LOCATION: 4
1 LOCATION: As is hydroxyethylene or statine
US-09-724-568-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURKENT FILING DATE: 2000-11-28

PRIOR PELICATION NUMBER: US 09/501,708

PRIOR FILING DATE: 2000-02-10

PRIOR APPLICATION NUMBER: 60/119,571

PRIOR APPLICATION NUMBER: 60/119,571

PRIOR APPLICATION NUMBER: 60/139,172

PRIOR FILING DATE: 1999-02-10

PRIOR FILING DATE: 1999-06-15

NUMBER: OF EQ ID NOS: 104

SEQ ID NO 81

LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, John P.
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guridpal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 81, Application US/09471669A
Patent No. 6830918
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
                                                                                                                                                                                                                                                                                                                                                     ; Sequence 81, Application US/09724566A; Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                              Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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VMXVAEF 7
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US-09-471-669A-81
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Gaps

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VS-09-583-110-5099

i Sequence 5099, Application US/09583110

j Patent No. 6699703

j Patent No. 699703

j GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

i TITLE OF INVENTION: Number: US/09/583,110

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

i PRIOR FILING DATE: 1998-05-12

i RING APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1998-05-12

i RING FILING DATE: 1998-05-12

i RING APPLICATION NUMBER: US 60/051,553

i RING APPLICATION NUMBER: US 60/051,553

i ENGINE APPLICATION NUMBER: US 60/051,553
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TITLE OF INVENTION: WXXCOCCUS xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 188
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                                                                                                                                                                                                                                                                            Score 24; DB 4; Length 188; Pred. No. 1.5e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 4; Length 335; 71.4%; Pred. No. 2.8e+02;
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Patent No. 6413521
GENERAL INFORMATION:
APPLICANT: MCMICHAEL-PHILLIPS et al.
TITLE OF INVENTION: Helminth Parasite Antigen with
TITLE OF INVENTION: Aminopeptidase-like Activity
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barbara G. Ernet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptococcus pneumoniae US-09-583-110-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Barbara G. Ernst
555 13TH STREET, NW
                                                                                                                                                                                                                                                                            82.8%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                 ; ORGANISM: Myxococcus xanthus US-09-902-540-14932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4.
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                                                                                                                                                                                                                                                                                                  Best Local Similarity
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US-08-637-670-40
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                                                                                                                              Sequence 7260, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

ITTLE OF INVENTION: UDGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

ITTLE OF INVENTION: UDGLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 2709.1002-001

CURRENT PELLING DATE: 2000-04-05

PRIOR PELLING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3800, Application US/09134000C

Sequence 3800, Application US/09134000C

Batent No. 6617156

GENERAL INPORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 3800

LENGTH: 194
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89;
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69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 4
Pred. No. 69;
0; Mismatches
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Pred. No. 8
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Patent No. 683347
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.1%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Proteus mirabilis
US-09-543-681A-7260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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112 VLSVAEF 118
                          1 VMXVAEF 7
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    VMXVAEF
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ORGANISM:
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JOANNA JANE
SUSAN BLIZABETH
RECOMBINANT DNA MOLECULES ENCODING
AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
VACCINES AGAINST HELMINTH INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECOMBINANT DNA MOLECULES ENCODING
AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
VACCINES AGAINST HELMINTH INFECTIONS
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                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 09-JAN-1995
CLASSIFICATION NUMBER: 08/08/335,844A
FILNG APPLICATION DATA:
APPLICATION NUMBER: 08/08/335,844A
FILNG APPLICATION DATE: 04-JAN-1995
FILNG APPLICATION DATE: 06-MAY-1993
FILNG APPLICATION NUMBER: GB 920936
FILNG DATE: 08-MAY-1992
ATPOINT APPLICATION NUMBER: 35,400
REGISTRATION NUMBER: 1181-223A
TELEPHONE: 02027783-6040
                                                                                                                                       ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 3; 1
Pred. No. 8.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09129366
Patent No. 6534638
GENERAL INFORMATION:
APPLICANT: GRAHAW, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MINDEPRINANT DNA MINDEPRINASE BEN
TITLE OF INVENTION: AMINOREPRINASE BEN
TITLE OF INVENTION: VACCINES AGAINST
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 972 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 783-6031
               APPLICANT: NEWTON, SUSAR
TITLE OF INVENTION: REC
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: VAC
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-335-844A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell,
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: ||||
542 VISVAEF 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D. C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-129-366-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION UNMER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4831
LENGTH: 927
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83.3%; Pred. No. 8.4e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 4; Length 620; 71.4%; Pred. No. 5.5e+02;
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      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08335844A
Patent No. 6065503
GENERAL INFORMATION:
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MONN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 71.4 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: [|[|
203 VISVAEF 209
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    MEDIUM TYPE:
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US-09-134-001C-4831
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US-08-335-844A-24
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Sequence 46, Application US/08456647B

Patent No. 5811516

GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg B.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: La Jolla
  Sequence 18, Application US/08456647B
Patent No. 5811516
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CARRESESEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PULICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
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57.1%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Best Local Similarity
                                                                                                                                                                                                                La Jolla
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                                                                                                                                                                                                                                STATE: CA
COUNTRY: US
ZIP: 92037
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US-08-456-647B-18
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GENERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREGMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1099-01-29
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 4; Length 972; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/129,366
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
                                                                                                                                                                                                PULASSIFILATION DATA:
PULASSIFILATION DATA:
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR PAPLICATION NUMBER: GB PCT/GB93/00943
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: GB 920936
FILING DATE: 08-MAY-1992
ATORNEY/AGENT INFORMATION:
NAME: ERNST, BATBATA G.
REFERENCE/DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 972 amino acids
amino acid
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SEQ ID NO 8879
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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542 VISVAEF 548
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US-09-489-039A-8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Patentin Release #1.0, Version #1.25

SOFTWARE:

RESULT 15

Gaps

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Score 23; DB 2; Length 54;
Pred. No. 72;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08237401A

Patent No. 5837448

GENERAL INFORMATION:

APPLICANT: Lember Ph.D. et al., Greg E.

ITILE OF INVENTION:

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELEPONE: (619) 678-509
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
US-08-237-401A-46
Sequence 46, Application US/08237401A
Patent No. 5837448
GENERAL INFORMATION:
                           LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                     79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 amino acids
                                                                                                                                                                                                  Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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              SEQUENCE CHARACTERISTICS
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-647B-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
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9 VMKIADF 15
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Best Local Similarity
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ZIP: 92037
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Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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US-08-456-647B-47

US-08-456-647B-47

Sequence 47, Application US/08456647B

Patent No. 5811516

GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg E.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BEACHLIN Release #1.0, Version #1.25

SOFTWARE: PEPLICATION DATA:

APPLICATION NUMBER: US/08/456,647B

FILING DATE: 02-4UN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/237,401

FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/884,486

FILING DATE: 15-MAY-1992

ATORNEY AGENT INFORMATION:

NAME: Wetherell Ph.D., John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 31,678

RELECHOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FAR-6099
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-UVN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
TELEFROME (619) 678-5099
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE GHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || :|:|
9 VMKIADF 15
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Gaps

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Sequence 1665, Application US/09248796A

Facer 1665, Application US/09248796A

Facer No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16636
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
VENTION: SF. a No. 6558910el Family of Taste Receptors
NCE: 02307E-098000US
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Pred. No. 72;
2; Mismatches 1; Indels
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Pred. No. 1e+02;
0; Mismatches 2; Indels
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
RECISTRATION NUMBER: 07251/007001
TELECOMMULICATION INFORMATION:
TELEPAX: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/09393634
Patent No. 6558910
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
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Adler, Jon Elliot
Ryba, Nick
Mueller, Ken
Hoon, Mark
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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9 VMKIADF 15
                                                                                                                                                                                                                                                                                                   linear
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FILE REFERENCE: 023
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APPLICANT:
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                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESCEE: 54
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
    APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET 4225 Executive Square, Suite 1400
CITY: La Jolla
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APPLICATION NUMBER: US/08/237,401A FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/884,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 54 amino acids
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Best Local Similarity 57.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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9 VMKIADF 15
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ZIP: 92037
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US-08-237-401A-47
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Gaps

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US-09-270-767-34950

Sequence 34950, Application US/09270767

Sequence 34950, Application US/09270767

Sequence 34950, Application US/09270767

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 34950

LENGTH: 203
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: Fille Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50167
LENGTH: 203
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
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Pred. No. 2.9e+02;
0; Mismatches 1; Indels
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                             Indels
    57.1%; Pred. No. 2.8e+02; ative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-34950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                           4; Conservative
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99 IMDVADF 105
    Best Local Similarity
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US-09-270-767-50167
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                           Matches
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 3642
LENGTH: 132
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Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 4; Length 90;
42.9%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 76
LENGTH: 90
                                                                                                                                                                                                                                         i LOCATION: (1)...(90)
i OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23;
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; Patent No. 6617156
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; ORGANISM: Drosophila melanogaster
US-09-270-767-41416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                              OTHER INFORMATION: human GR22
NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                :: :|||
11 ILAIAEF 17
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9 LMDIAEF 15
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Matches 4; Conserv
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US-09-270-767-41416
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US-09-134-000C-3642
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LENGTH: 193
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOHAMMADI,
APPLICANT: MOHAMMADI,
APPLICANT: MOHAMMADI,
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: 08/0964,526
CURRENT FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 13
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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195-01-191A-31
25 Sequence 31, Application US/08701191A
25 Sequence 10-594242B
36 GENERAL INFORMATION:
APPLICANT: Mosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
31TILE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 4; Length 299;
Pred. No. 4.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%; Score 23; DB 2; I 57.1%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1955-0440
TELEFAX: (213) 955-0440
TELEFAX: (713) 955-0410
TELEFAX: (713) 955-0410
TELEFAX: (713) 955-0410
TELEFAX: (713) 955-0410
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13, Application US/09664526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                          299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-09-664-526-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 VMKIADF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :|:|
172 VMKIADF 178
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTY PAPLICATION NUMBER: US/09/270,767

CURRENT PAPLICATION DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
US-00-701-191A-13

iSequence 13, Application US/08701191A

iPatent No. 5942428

GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,

APPLICANT: LOS DANGERS:

ADDRESSE: Joyn & Lyon

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

CITY: Los Angeles

STREET: Galifornia

COUNTRY: US.A.

ABDIUM TYPE: S. Diskette, 1.44 Mb

MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                           Score 23; DB 4; Length 285;
Pred. No. 4.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 285;
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Pred. No. 4.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
UURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
                                                                                                                                                        TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-270-767-32289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Drosophila melanogaster
US-09-270-767-47506
                                                                                                                                                                                                                                                  79.3%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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US-09-270-767-47506
                                                                                                            SEQ ID NO 32289
LENGTH: 285
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LENGTH: 285
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th 79.3%;
Similarity 57.1%;
4; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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181 VMKIADF 187
                          Query Match
Best Local Similarity
Matches 4; Conserv
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STRANDEDNESS: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WOHADAMADI, MOCSA
APPLICANT: WOHADAMADI, O'STEVAN R.
TITLE OF INVENTION: CRYSTALS O'R THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REPERENCE: 038602/0847
CURRENT APPLICATION UNMBER: US/09/664,526
CURRENT FILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-11-09
PRIOR PILING DATE: 1996-08-18
PRIOR APPLICATION NUMBER: 09/189,809
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 31
LENGTH: 300
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      OF NON-INSULIN RECEPTOR TYROSINE KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 2; I
Pred. No. 4.5e+02;
                                                                             CORRESPUNDENCE ADMINEST
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: BECAGABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BCATSEQ for Windows 2.0
COMPUTER: PREAEMS for Windows 2.0
CONFURER: PREAEMS for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION NUMBER: US/08/701,191A
FILING DATE: RICHARD J.
REPERENCE/AGENT INFORMATION:
NAME: Warburg, Richard J.
RELEPROMENIONINHER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 227/088
TELEPROMENICATION INFORMATION:
TELEPROMENICATION INFORMATION:
TELEPROMENICATION TOWATION:
TELEPROMENICATION TOWATION
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US-09-664-526-31
; Sequence 31, Application US/09664526
; Detent No. 6682921
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 300 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-664-526-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :|:|
172 VMKIADF 178
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                                                                                                                                                                                                                                                 Sequence 9, Application US/08701191A
Sequence 9, Application US/08701191A
Patent No. 5942428
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MODE MANDERMEDING CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSED: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.3%; Score 23; DB 2; Length 309; Best Local Similarity 57.1%; Pred. No. 4.6e+02; Matches 4; Conservative 2; Mismatches 1; Indels
Score 23; DB 4; Length 300;
Pred. No. 4.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: August 21, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
US-09-664-526-9
; Sequence 9, Application US/09664526
; Patent No. 6682921
; PAPLICANT: MOHAMMADI, MOOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPEROR/OFOCKT NUMBER: 227/(
TELECOMMUNICATION INFORMATION:
TELERAX: (213) 955-0440
TELEX: 67-310
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 anino acids
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Length 310;

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79.3%;
57.1%;
                                                                                      Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
h MOLECULE TYPE: protein
h HYPOTHETICAL: NO
US-08-701-191A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                               181 VMKIADF 187
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                                                                                                                                                                                                                                                                                                        US-08-701-191A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-701-191A-6
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             APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08701191A
Patent No. 5942428
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: MOMORA Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 4; Length 309;
Pred. No. 4.6e+02;
2; Mismatches 1; Indels
                                                                           FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR PILING DATE: 1998-11-09
PRIOR PELING DATE: 1996-11-09
PRIOR FILING DATE: 1996-08-21
NUMBER: OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTESED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: August 21, 1996
CLASSIFICATION 530
PROGRAPHICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
FILING DATE:
FILING DATE:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELECOMMUNICATION INFORMATION:
TELEFANE: (213) 489-1600
TELEFANE: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700`
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
  SCHLESSINGER, JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
US-08-701-191A-1
                                                                                                                                                                                                                                                                                                        LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                    US-09-664-526-9
                                                                                                                                                                                                                                                                               SEQ ID NO 9
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                                                                                                                                                                                                                              ; Sequence 6, Application US/08701191A; Sequence 6, Application US/08701191A; Sequence 6, Application US/08701191A; Patent No. 5942428; Patent No. 5942428; Patent No. 5942428; Patent Information: Applicant: Moosa Mohammadi, Joseph Schlessinger, APPLICANT: and Stevan R. Hubbard TTILE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon STREET: 613 West Fifth Street
; STREET: Suite 4700
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Pred. No. 4.6e+02;
2; Mismatches 1; Indels
Score 23; DB 2; I
Pred. No. 4.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: August 21, 1996
CLASSIFICATION 5730
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
US-08-701-191A-7
; Sequence 7, Application US/08701191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: MCKERSHAM, JOHN A.
APPLICANT: SHOWALTER, RICHARD
APPLICANT: PRASST, CAWRAN V.
APPLICANT: PRASST, CAWRAN V.
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GENERACK, BARBARA
APPLICANT: KAN, CHEN-CHEN
APPLICANT: WROCZKOWSKI, BARBARA
APPLICANT: WILAFRANCA, J. BRNEST
APPLICANT: VILLAFRANCA, J. BRNEST
APPLICANT: VILLAFRANCA, J. BRNEST
APPLICANT: WINSTHON: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: MODIFICATIONS OF USE
TITLE OF INVENTION: WETHOUS OF USE
CURRENT APPLICATION NUMBER: US/09/390,326
CURRENT APPLICATION NUMBER: US/09/390,326
SCTURRENT PILING DATE: 1999-09-07
SOFTWARE: PAEGIL NOS: 12
SOFTWARE: PAEGIL NOS: 12
SOFTWARE: PAEGIL NOS: 12
SOFTWARE: PAEGIL NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23, DB 2; Length 310;
Pred. No. 4.6e+02;
2; Mismatches 1; Indels
MEDIUM TYPE: 3.5 CCCOMPUTER: BLOOMER STORED COMPUTER: IBM Compactable COMPUTER: IBM Compactable OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASSES for Windows 2.0 CURRENT APPLICATION NATA: APPLICATION NATA: APPLICATION NUMBER: US/08/701,191A PILING DATE: AUGUST 21, 1996 CLASSIFICATION: 530 PRIOR APPLICATION NUMBER: SAPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Warburgy, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 227/088 TELEFHONE: (213) 489-1600 TELEFAN: (213) 955-0440 TELEFAN: (7-3510 NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 310 amino acids TYPE: amino acid STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09390326
Patent No. 6316603
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Best Local Similarity 57.1%;
Matches 4; Conservative 5
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181 VMKIADF 187
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-390-326-7
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           GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
TITLE OF INVENTION: CRYSTALS OF THA
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
STREET: Suite 4700
CITY: Los Angeles
STARET: California
CONDTRY: U.S.A.
ZIP: 90071-206
CONDTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.49 Mb
MEDIUM TYPE: ACCOMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: RateSed for Windows 2.0
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
US-08-701-191A-8
i Sequence 8, Application US/08701191A
i Patent No. 5942428
i GENERAL INFORMATION:
i APPLICANT: moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
i TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE
i NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELEFONMUNICATION INFORMATION:
TELEFONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFX: 67-3510
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-701-191A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
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181 VMKIADF 187
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  ; Patent No. 5942428
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Gaps

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us-uy-ee4-126-8

Sequence 8, Application US/09664526

Patent No. 6682921

GENERAL INFORMATION:

APPLICANT: MOHAMMADI, MOOSA

APPLICANT: HUBBARD, STEVAN R.

TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: 09/188,809

PRIOR PELLING DATE: 1998-11-09

PRIOR PELLING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTION OF SEQ ID NOS: 41

SEQ ID NO 8

LENGTH: 310

TYPE: PRT
                           PATENT NO. 6882921
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: MCHAMMADI, MCOSA
TITLE OF INVENTION: CRYSTALES OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: 08/0964,526
CURRENT FILING DATE: 1090-09-18
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/189,909
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR PILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 7
LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
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Pred. No. 4.6e+02
2; Mismatches
Sequence 7, Application US/09664526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/09939833
; Patent No. 6753416
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Best Local Similarity 57.1%;
Matches 4; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WICKERSHAM, JOHN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: WICKERSHAM, JOHN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-664-526-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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181 VMKIADF 187
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181 VMKIADF 187
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US-09-939-833-7
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Sequence 6, Application US/09664526

Sequence 7, Application US/09664526

GENERAL INFORMATION:
APPLICANT: MOTAMMADI, MOOSA

APPLICANT: GCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.

TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT APPLICATION NUMBER: US/09/664,526

CURRENT PILING DATE: 1998-11-09

PRIOR PLILING DATE: 1998-11-09

PRIOR APPLICATION NUMBER: 08/701,191

PRIOR APPLICATION NUMBER: 08/701,191

SOFTWARE: PATCHILL Ver. 2.1

SOFTWARE: PATCHILL Ver. 2.1

SOFTWARE: PATCHILL Ver. 2.1
                                                                                                               ## Sequence 1, Application US/09664526

## Sequence 1, Application US/09664526

## Patent No. 6682921

## Patent No. 668292

## Patent No. 66829

## Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 4; Length 310; 57.1%; Pred. No. 4.6e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.3%; Score 23; DB 4; Length 310; 57.1%; Pred. No. 4.6e+02; ive 2; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-664-526-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | :|:|
181 VMKIADF 187
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181 VMKIADF 187
181 VMKIADF 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF 7
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US-09-664-526-6
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US-09-664-526-7
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RESULT 47
US-08-278-089A-17
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| Sequence 7, Application US/09506906
| Patent No. 6784285
| GENERAL INFORMATION:
| APPLICANT: MCIGUE, MICHELE A. APPLICANT: WICKERSHAM, JOHN A. APPLICANT: WICKERSHAM, JOHN A. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: TEMPCYZK-RUSSEL, ANNA APPLICANT: TEMPCYZK-RUSSEL, ANNA APPLICANT: TEMPCYZK-RUSSEL, APPLICANT: MRCCXCKOWSKI, BARBARA APPLICANT: NUMBER: US/09/506,906
| TITLE REFRENCE: 1012-0016US | TITLE REFRENCE: 1012-0016US | TITLE REFRENCE: 1012-0016US |
| TITLE OF INVENTION: MCHADER: US/09/300,326 |
| PRIOR PILING DATE: 2000-02-18 |
| PRIOR FILING DATE: 1999-09-07 |
| SEQTIMARE: PATENTIN VET: 2.0 |
| SEMICIPAL OF THE PATENTIN VET: 2.0 |
| SEMICANTIN VET: 2.0 |
APPLICANT: BINKO, CHRIS
APPLICANT: SHOWALTER, RICHARD
APPLICANT: PARASI, CAMANAN V.
APPLICANT: PARASI, CANNAN V.
APPLICANT: TEMPOCZK-GUSSEL, ANNA
APPLICANT: GEHRING, MICHAEL R.
APPLICANT: MRCHAEL R.
APPLICANT: MANACKOWSKI, BARBARA
APPLICANT: WILLAFRANCA, J. ERNEST
APPLICANT: APPELT, KGZYSZTOF
TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 0125-0016US
CURRENT FILING DATE: 1099-09
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PARENTIN VET. 2.0
SSOFTWARE: PARENTIN VET. 2.0
SSOFTWARE: PARENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 4; Length 310; 57.1%; Pred. No. 4.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.1
Matches 4; Conservative
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CRGANISM: Homo sapiens
US-09-506-906-7
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ORGANISM: Homo sapiens
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181 VMKIADF 187
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181 VMKIADF 187
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US-09-506-906-7
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Sequence 2. Application US/09664526
Sequence 2. Application US/09664526
Sequence 2. Application US/09664526
GENERAL INFORMATION:
APPLICANT: MOHAMADI, MOOSA
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0867
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 2000-09-18
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                                                                                                             Sequence 2, Application US/08701191A
Patent No. 5942428
GENERAL INFORMATION:
APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 23; DB 2; Length 315; 57.1%; Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: 1.8 Storage COMPUTER: 1.8 STORAGE COMPUTER: 1.8 STORAGE COMPUTER: 1.8 COMPATIBLE COMPUTER: 1.8 P.C. DOS 5.0 SOFTWARE: FASTSED for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/701,191A FILING DATE: AUGUST 21, 1996 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/11/10 DATE: ATTORNEY/AGENT INFORMATION: NAME: WAZDIER, REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 227/088 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELEC
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: sincl
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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186 VMKIADF 192
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08838957A

Patent No. 598187

GENERAL INFORMATION:
APPLICANT: Breitman, Martin L.
APPLICANT: Dumont, Daniel J.
TITLE OF INVENTION:
NO. 598187el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 4.7e+02;
2; Mismatches 1; Indels
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APPLICATION NUMBER: US/08/838,957A

FILING DATE: 23-APR-1997

CLASSIFICATION * 435

ATTORNEY/AGENT INFORMATION:

NAME: Kurdydyk, Linda M.

REGISTRATION NUMBER: 3153-212

TELEPHONE: (416) 364-731

TELEPHONE: (416) 364-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 2; I
Pred. No. 4.7e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 313 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                        313 amino acids
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: FlgM
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159 VMKIADF 165
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Best Local Similarity
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                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDN
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                                                                                                                                                                                                                                i IMMEDIATE SOURCE:
CLONE: FlgM
US-08-278-089A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-838-957A-16
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                                                                                 LENGTH:
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US-09-134-001C-5567

US-09-134-001C-5567

Sequence 5567, Application US/09134001C

SEQUENCE OF INVENTION:

TITLE OF INVENTION:

SEQUENCE RELATING TO STAPHYLOCCCUS

CURRENT APPLICATION NUMBER: US 60/064, 964

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

SEQ ID NOS: 5674

LENGTH: 344
                                                                                                                                                                                    Sequence 10, Application US/09664526;
Patent No. 668291
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WOHAMMADI, MOOSA
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION UNMBER: 09/0864,526
CURRENT FILING DATE: 12998-11-09
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/189,809
PRIOR APPLICATION NUMBER: 09/189,809
PRIOR APPLICATION NUMBER: 09/109
PRIOR FILING DATE: 1396-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 10
LENGTH: 318
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Pred. No. 5.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 57.1%; Pred. No. 4.8e+02; 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , TYPE: PRT
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 54
US-08-701-191A-3
; Sequence 3, Application US/08701191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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303 VMIIADF 309
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188 VMKIADF 194
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188 VMKIADF 194
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Best Local Similarity
Matches 4; Conserv
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      1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 51
US-08-701-191A-10
i Sequence 10. Application US/08701191A
i Sequence 10. Application US/08701191A
i Patent No. 5942428
i GENERAL INFORMATION:
i APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: Woosa Mohammadi, Joseph Schlessinger,
APPLICANT: Woosa Mohammadi, Joseph Schlessinger,
STREET: Suite 4700
CITY: Los Angeles
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö,
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Pred. No. 4.7e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,327
FR: 227/088
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TELEFAX: (213) 489-1600
TELEX: (213) 955-040
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TYPE: 318 amino ocity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :|:|
186 VMKIADF 192
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                                                                                                                                                                                                                   LENGTH: 315
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                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: protein encoded by recombinant baculovirus
US-09-664-526-3
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APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Addic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESSONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      '; Sequence 8, Application US/08885418
; Patent No. 5925528
; GENERAL INFORMATION:
; APPLICANT: Chiu, Ing-Ming
; APPLICANT: Poulin, Matthew L
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 378;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                         Length 351;
                                                                                                                                                                                                                     Score 23, DB 4, Length 351
Pred. No. 5.3e+02,
2, Mismatches 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08070165F
Patent No. 5750365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.38;
                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                       Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 43210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                          222 VMKIADF 228
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Best Local Similarity
Matches 4; Conserv
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US-08-070-165F-8
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APPLICANT: MCHAMALI, MCOSA
APPLICANT: MCHAMALI, MCOSA
APPLICANT: MCHAMALI, MCOSA
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRESTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REPERENCE: 038602/0847
CURRENT PILING DATE: 1000-09-18
PRIOR PLING DATE: 1998-11-09
PRIOR FLING DATE: 1998-11-09
PRIOR FLING DATE: 1998-11-09
PRIOR FLING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
           GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
ITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 351;
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                                                                                                                                                                                                              STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTEN YERDADALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTEN: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/701,191A FILING DATE: August 21, 1996 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 227/
TELECOMMUNICATION INFORMATION:
TELEPRONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09664526
; Patent No. 6682921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Best Local 4; Conservative
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222 VMKIADF 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-701-191A-3
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR RILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                        Gaps
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APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Chou, Ing-Ming
APPLICANT: Chou, Ing-Ming
ITILE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
INUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
CITY: Columbus
CITY: Columbus
STATE: Ohio
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 23; DB 2; Length 388; 57.1%; Pred. No. 5.9e+02; ive 2; Mismatches 1; Indels
                                                        Score 23; DB 1; Length 388; Pred. No. 5.9e+02;
                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 43210

COMPUTER READABLE FORM:
MEDIUM TYPER Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPERTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/885,418
                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 60
US-092-252-991A-28422
; Sequence 28422, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08885418
Patent No. 5925528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                        79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 388 amino acids TYPE: amino acid
                                                        Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                               || :|:|
204 VMKIADF 210
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204 VMKIADF 210
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              US-08-070-165F-4
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US-08-885-418-4
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: $20.5 Davis Medical Research Center, 480 West
STREET: $0.0 Davis Medical Research Center, 480 West
STREET: $10.0 Davis Medical Research Computer Readable Form:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (614)-293-693
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LEMGTH: STR aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08070165F
Patent No. 5750365
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 2; Length 378;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALLY
FILING DATE:
CLASSIFTCATION: 435
CLASSIFTCATION: 435
TELECOMMUNICATION INFORMATION:
TELEPRAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acids
TOPE: TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 378 amino acids
amino acid
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Best Local Similarity 57.1°
"...hea 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-885-418-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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197 VMKIADF 203
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US-08-070-165F-4
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Gaps
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APPLICANT: Human Genome Sciences, Inc. et al.

TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

FILE REFERENCE: PB484
CURRENT APPLICATION WUMBER: US/10/138,701
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION WUMBER: US/09/512,255A
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1098-09-01
PRIOR PLILOR DATE: 1098-09-01
PRIOR PLILOR DATE: 1998-09-01
PRIOR PLILOR DATE: 1999-08-31
PRIOR PLILOR DATE: 1999-08-31
PRIOR PLILOR DATE: 1999-08-31
PRIOR PLILOR DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 421
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GENEMAL INVORVATION:

GENEMAL INVORVATION:

TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

FILE REFERENCE: P8484

CURRENT APPLICATION NUMBER: US/10/138,701

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: US 60/098,964

PRIOR APPLICATION NUMBER: US 60/099,861

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1999-01-05

PRIOR FILING DATE: 1999-01-05

PRIOR FILING DATE: 1997-10-20

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PATENTIN NUMBER: DATE: 1997-10-20

SEQ ID NO 22

LENGTH: 41
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Pred. No. 6.4e+02;
0; Mismatches 1; Indels
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Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-138-701-22; Sequence 22, Application US/10138701
; Sequence 22, Application US/10138701
; Datent No. 6753149
; GENERAL INFORMATION:
                                                                                                          Sequence 8, Application US/10138701
Patent No. 6753149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Staphylococcus aureus
US-10-138-701-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus US-10-138-701-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3
Best Local Similarity 83.3
Matches 5; Conservative
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  336 MHVAEF 341
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                                                                                     US-10-138-701-8
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 43247, Application US/09270767

Sequence 43247, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT ELLING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 43247

LENGTH: 412
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Patent No. 6703492
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: 60/9/710,279
CURRENT PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
US-09-710-279-1818
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                                                                                                                             DB 4; Length 397;
6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 4; Length 412; 71.4%; Pred. No. 6.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                           1; Indels
                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43247
                                                                                                                               Score 23;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster
                       LENGTH: 397
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                               79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3.
                                                                                                                                                    Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 VMLVVEF 182
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259 MAIAEF 264
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                                                                                 US-09-252-991A-28422
                                                                                                                                                                                                                                                                                                                                  RESULT 61
US-09-270-767-43247
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US-09-710-279-1818
SEQ ID NO 28422
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                                                                                                                                    Query Match
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Gaps

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2 MXVAEF 7

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Sequence 7991, Application US/09328352

Patent No. 656298

GENERAL INFORMATION:

APPLICANT: GALY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7991

LENGTH: 613
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Pred. No. 9.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 612;
                                 TYROSINE KINASE AND LIGAND AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 2; Ler
71.4%; Pred. No. 9.6e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
                BSK RECEPTOR LIKE
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BSK RECEPTOR TITLE OF INVENTION: TYROSINE KIN TITLE OF INVENTION: USB IN DIAGNI TITLE OF INVENTION: USB IN DIAGNI TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-7991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 VMIVTEF 327
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: USA
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                                                                                                                                                                                                                        COUNTRY:
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                                                               RESULT 65
US-09-134-001C-4257
Sequence 4257, Application US/09134001C
Patent No. 6380370
Fatent No. 6380370
Fatent No. 6380370
Fatent No. 6380370
FILE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PELICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PLILING DATE: 1997-08-14
PRIOR PLILING DATE: 1997-08-14
FRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4257
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31250, Application US/09252991A;
Sequence 31250, Application US/09252991A;
Patent No. 6551795;
GENERAL INFORMATION:
TITLE OF INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TILLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TILLE OF INVENTION: AND THE NOT APPLICATION NUMBER: US/09/252,991A;
CURRENT APPLICATION NUMBER: US 60/074,788;
PRIOR PILING DATE: 1998-02-18;
PRIOR PILING DATE: 1998-07-27;
NUMBER OF SEQ ID NOS: 33142;
SEQ ID NO 31250;
LENGTH: 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS, APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 3; I
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
JS-09-252-991A-31250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.3
Best Local Similarity 83.3
Matches 5; Conservative
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433 VLGIAEF 439
336 MHVAEF 341
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Sequence 6, Application US/08070165F

Patent No. 2750365

GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matchew L
TILE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ing-Ming Chiu
STREET: $2,052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
COMPTIER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFREENCE/DOCKET NUMBER: 3,113
REFREENCE/DOCKET NUMBER: CH-165
TELECOMMUNICATION INFORMATION:
TELEFHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 1; I
Pred. No. 1.2e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
TYPE: amino acid
                        4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: $10-655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 729 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
         Aborton
STREET: 4500
CITY: Emeryville
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 VMKIADF 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VMXVAEF 7
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  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-640-029-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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APPLICANT: Kiefer, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                             US-08-471-570-10

Sequence 10, Application US/08471570

Sequence 10, Application US/08471570

PARENT NO. 5750371

APPLICANT: IGARASHI, Koichi
APPLICANT: SENCO, Masaharu

APPLICANT: WATNANAE, Tatsuya

TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVIO G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

ADDRESSEE: CUSHMAN

STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 1; Length 652;
Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATFORNEY/AGENT INPORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REGISTRATION NUMBER: 29822
REGISTRATION NUMBER: 29822
REFERENCE/POCKET NUMBER: 29822
RELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 70
US-07-640-029-3
; Sequence 3, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 652 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-471-570-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :|:|
523 VMKIADF 529
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53 IMELAEF 59
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RESULT 74
US-08-070-165F-10
is Sequence 10, Application US/08070165F
sequence 10, Ind., Ing., 
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC computeR
COMPUTER: IBM PC computeR
COMPUTER: IBM PC computeR
COMPUTER: IBM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
FILING DATE:
CLASSIFICATION: 435
TELECOMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 731 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :|:|
545 VMKIADF 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-921-807B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 72
US-08-88-418-6
i Sequence 6, Application US/08885418
i Patent No. 525528
i GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
ITTLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
STREET: Olumbus
STREET: Ohio.
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                                                                                                                                                                Length 729;
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Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGUERO S. APPLICATION US/07921807B
PATENT NO. 5474914
GENERAL INFORMATION:
APPLICANT: SPAFE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 23; DB 1; I 57.1%; Pred. No. 1.2e+03; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 729 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-885-418-6
                                                                                                                                                                                                                                             Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-165F-6
                                                                                                                                    Query Match
Best Local Similarity
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547 VMKIADF 553
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547 VMKIADF 553
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US-07-921-807B-5
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Patent No. 6255454
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Raibfer, Michael C.
APPLICANT: Philip, Barr J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S2052 Davis Medical Research Center, 480 West
                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEFFAX: (614)-293-8093
TELEFAX: (614)-293-8093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 0165.004
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
                                                                    ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiron Corporation
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                 JACTERISTICS:
JACTERISTICS:
TYPE: amino acid
TOPOLOGY: 11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :|:|
549 VMKIADF 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Chiron
STREET: 4560 Hort
CITY: Emeryville
STATE: CA
    STREET: 9tm
STREET: Olumbus
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VMXVAEF 7
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                                       CITY: Col
STATE: Oh
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-885-418-10
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Patent No. 592528
GENERAL INFORMATION:
APPLICANT: Chulin, Matthew L
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
79.3%; Score 23; DB 1; Length 731; 57.1%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 731;
                                                                                                                                                                                                  Sequence 5, Application US/08441944A

Patent No. 5767250

GENERAL INFORMATION:

APPLICANT: SPAETE, RICHARD

TITLE OF INVENTION:

TITLE OF INVENTION: OF VIRAL PROTEINS

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: 4560 Horton Street - R440

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUUNTER: USA

ZIP: 94608-2916

COUNTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/41,944A
FILING DATE: 16-MAY-1995
CLASSITCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/41,907
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0209.001
TELECOMMUNICATION NUMBER: 75,113
REFERENCE/DOCKET NUMBER: 75,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 1; I
57.1%; Pred. No. 1.2e+03;
                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 731 amino acids
TYPE: amino acid
STRANDEDNESS: single
                Best Local Similarity 57.1 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                    || :|:|
549 VMKIADF 555
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                                                                           1 VMXVAEF 7
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                                                                                                                                                                           RESULT 75
US-08-441-944A-5
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US-08-885-418-10
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Query Match
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79.3%; Score 23; DB 1; Length 733; 57.1%; Pred. No. 1.2e+03; tive 2; Mismatches 1; Indels
                                                                                                                                                      COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAEENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,807
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SPAETE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
TITLE OF INVENTION: OF VIRAL PROTEINS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: CHIRON CORPORATION STREET: 4560 Horton Street - R440 CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Smeryville
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08441944A Patent No. 5767250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (510) 655-3542
INPORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.14
- Then 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :|:|
547 VMKIADF 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-921-807B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kiefer, Michael C.
APPLICANT: Kiefer, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OP SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Emeryville
CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 1; Length 733; 57.1%; Pred. No. 1.2e+03; ive 2; Mismatches 1; Indels
                                                                                                                     Length 731;
                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUDNICKS: USEN CONFUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ENDRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: CH-165
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 4:
SPOITENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/07921807B

Patent No. 5474914

GENERAL INFORMATION:

APPLICATE: SPAETE, RICHARD

ITTLE OF INVENTION: METHOD OF INCREASING EXPRESSION
                                                                                                                  Score 23; DB 3; Pred. No. 1.2e+03;
                                                                                                                  Query Match 79.3%; Score 23; DB Best Local Similarity 57.1%; Pred. No. 1.2e Matches 4; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                     RESULT 78
US-07-640-029-4
; Sequence 4, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-640-029-4
                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-439-992A-3
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545 VMKIADF 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 79
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Gaps

09730329-60ed.rai

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Sequence 7119, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,755
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                    Sequence 8, Application US/08471570
Patent No. 5750371
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SENCO, Macaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS OF THE CONTRESPONDENCE ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETHERE V
REGISTRATION NUMBER: 29822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street CITY: Boston STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :|:|
640 VMKIADF 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 83
US-09-949-016-7119
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Patent No. 625444

GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Pablo, Valenzuela D.T.
APPLICANT: Philip, Barr J.
ITILE OF INVENTION: Expression and Use of Human Fibroblast
ITILE OF INVENTION: Receptor
NUMBER OP SEQUENCES: 12
CORRESPONDENCE S: 12
ADDRESSE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 23; DB 1; Length 733; 57.1%; Pred. No. 1.2e+03; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23, DB 3; Length 733; Pred. No. 1.2e+03; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USER STATES OF THE ST
                      REFERENCE/DOCKET NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%;
57.1%;
                                                                                                                                                                                                      LENGTH: 733 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 733 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :|:|
547 VMKIADF 553
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USA
                                                                                                                                                                                                                                                                                                                                                             US-08-441-944A-6
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US-08-439-992A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-439-992A-4
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Antonius
APPLICANT: Bazan, Theodore R.
APPLICANT: Razelelin, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/09/173,151A
FILING DATE: 14-0CT-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U$ 60/065,776
PRIOR APPLICATION NUMBER: U$ 60/078,008
FILING DATE: 17-NOV-1997
PRIOR APPLICATION NUMBER: U$ 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION NUMBER: U$ 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION NUMBER: U$ 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: U$ 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: U$ 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: U$ 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: U$ 60/062,066
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: U$ 60/062,066
FILING DATE: 18-MAR-1997
ATTONENEY/AGENT INPORMATION:
NUMBE: US-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34,090
FR: DX0767X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
REJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             US-09-173-151A-33
; Sequence 33, Application US/09173151A
; Patent No. 6326472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFRENCE/DOCKET NUMBER: DX07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
                     624 VMKIADF 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF 7
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 84
US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; TAPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; TITLE OF CHOUNDRODYSPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 801;
                                                                                                                                                                                                                                                           Length 795;
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                                                                                                                                                                                                                                                                                                        1: Indels
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                                                                                                                                                                                                                                                        79.3%; Score 23; DB 4; I 57.1%; Pred. No. 1.3e+03; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7119
LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-383-630-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1.
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   619 VMKIADF 625
                                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF 7
                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                             US-09-949-016-7119
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1 VMXVAEF 7

625 VMKIADF 631

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US-09-949-016-10904

| Sequence 10904, Application US/09949016
| GENERAL INFORMATION:
| APPLICANT: VERYIEN: J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| WIMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 10904 |
| LENGTH: 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 816;
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                                                                            COUNTRI: USANGE COMPUTER: USANGE COMPUTER: 194608
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: CH-165
TELECOMMUNICATION NIPORMATION:
TELECOMMUNICATION NIPORMATION:
TELECOMMUNICATION NIPORMATION:
TELECOMMUNICATION NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: B16 amino acids
TUNDER AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3%; Score 23; DB 1; I Best Local Similarity 57.1%; Pred. No. 1.3e+03; Matches 4; Conservative 2; Mismatches 1.
4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 816 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-07-640-029-1
                     CITY: Emeryville
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 VMKIADF 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-10904
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US-07-640-029-1
; Sequence 1, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Valenzuela, Fablo D.T.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; TITLE OF SEQUENCES: 12
; TOWNERS OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: «UKNOWN>
FILING DATE: «UNKNOWN>
FILING DATE: «UNKNOWN>
FILING DATE: «UNKNOWN>
APPLICATION NUMBER: «10 NUMBER: AUKNOWN>
FILING DATE: «UNKNOWN>
FILING DATE: «UNKNOWN>
APPLICATION NUMBER: 33,883
REGISTRATION NUMBER: 33,883
REGISTRATION NUMBER: 34,62/2
TELECOMMUNICATION INFORMATION:
                                                                         BESUL: 8-50-3

18-09-383-630-3

1 Sequence 3, Application US/09383630A

2 Fatent No. 6256532

2 GENERAL INFORMATION:

APPLICANT: ATNEY YAYON et al.

TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH

CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 806;
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Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-383-630-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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630 VMKIADF 636
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                                                                    RESULT 86
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PAPLICATION NUMBER: US/07/921,807B
PILING DATE: 29-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFERNICE/DOCKET NUMBER: 0209.001
TELEPHONE: (510) 601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08441944A Patent No. 5767250
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           820 amino acids
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Best Local Similarity 57.11
Lag 4; Conservative
CURRENT APPLICATION DATA:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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634 VMKIADF 640
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                                                                                                                                                               OFFICANT: Valentium:
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STRIE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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57.1%; Pred. No. 1.3e+03;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Second | S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/640,029

FILING DATE: 19910111

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: McClung, Barbara G.

REGISTRATION NUMBER: 33,113

REGISTRATION NUMBER: 33,113

REGISTRATION NUMBER: 31,12

REGISTRATION NUMBER: 31,12

REGISTRATION NUMBER: 31,13

REGISTRATION NUMBER: 31,13

REGISTRATION NUMBER: 10-650-3542

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 817 amino acids

TYPE: AMINO ACID

STRANDEDNESS: alingle

TOPOLOGY: linear:

TOPOLOGY: linear:

TOPOLOGY: linear:

TOPOLOGY: linear:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                          US-07-640-029-2; Sequence 2, Application US/07640029; Patent No. 5229501; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-07-640-029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:|
632 VMKIADF 638
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79.3%; Score 23; DB 1; Length 820; 57.1%; Pred. No. 1.3e+03; tive 2; Mismatches 1; Indels
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APPLICANT: SPAETE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
TUTLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON Street - R440
CITY: EMELYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: FULLDOS/MS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: US/07/921,807
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,807
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
FEGESTRATION NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER STICS:
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TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Hotton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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Patent No. 5863888
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPLICANT: Crunley, Greg
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CTTY: Callegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3%; Score 23; DB 3; Length 820; Best Local Similarity 57.1%; Pred. No. 1.3e+03; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Date IDMS-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REFERENCE/DOCKET NUMBER: 0165.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEFRANCE (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LPMSTH: 820 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 VMKIADF 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: C
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                                                                                     79.3%; Score 23; DB 1; Length 820; 57.1%; Pred. No. 1.3e+03; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yayon, Avner
APPLICANT: Yayon, Avner
APPLICANT: Klagabrun, Michael
APPLICANT: Leder, Philip
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
TITLE OF INVENTION: FACTOR RECEPTOR
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WACADERIECT (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/166,717D
FILING DATE: 12/14/93
CLASSIPICATION 1435
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 07/631,717
FILING DATE: 12/20/90
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kristina Bieker-Brady
REGISTRATION WINBER: 39,109
REFERENCE/DOCKET NUMBER: 00383/017002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08439992A
Patent No. 6255454
GENERAL INFORMATION:
APPLICANT: Fafer, Michael C.
APPLICANT: Pablo, Valenzuela D.T.
                                                                                                                                                                                                                                                                                            US-08-166-717D-6
; Sequence 6, Application US/08166717D
Patent No. 5789182
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENČE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 723-8962
                                                                                     Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-166-717D-6
                                                                                                                                                                                             || :|:|
634 VMKIADF 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634 VMKIADF 640
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US-08-439-992A-1
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Gaps

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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington a ZIP: 22202
ZIP: 22202
ZIP: 22202
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: FLOPPY disk COMPUTER: FLOPPY DECOMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/997,133
FILING DATE: 28-DEC-1992
CLASSIFTCATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5288855man F.
REGISTRATION: NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-226-0
TELECOMMUNICATION NUMBER: 769-226-0
TELECOMMUNICATION NUMBER: 769-226-0
TELECOMMUNICATION NUMBER: 769-226-0
TELECOMMUNICATION NUMBER: 769-226-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 1; Length 822;
Pred. No. 1.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                           Length 821;
                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bergonzoni, Laura
APPLICANT: Baccoli, Guy
APPLICANT: Isacchi, Annoella
APPLICANT: Sarmientos, Romeo
APPLICANT: Sarmientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Pibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                         Score 23; DB 3; I
Pred. No. 1.3e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07997133
Patent No. 5288855
GENERAL INFORMATION:
                  LENGTH: 821 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-323-430-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative 2
                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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(703)486-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 822 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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639 VMKIADF 645
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636 VMKIADF 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA

CUUNTRY: USA

ZIP: 19426

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/323,430

FILING DATE: US/08/323,430

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/549,587

FILING DATE: 06-JUL-1990

ATTORNEY AGENT INFORMATION:

NAME: Goodman, Rosanne

REGISTRATION NUMBER: 32,534

REFERENCE/DOCKET NUMBER: 32,534

REJERPHONE: (215) 454-3808

INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
; Sequence 13, Application US/08323430; Patent No. 6344546; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :|:|
639 VMKIADF 645
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US-08-323-430-13
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-441-944A-4

1 Sequence 4, Application US/0844194A

1 Sequence 4, Application US/0844194A

1 Sequence 4, Application US/0844194A

2 Sequence 4, Application US/0844194A

2 SEQUENCE:
2 SEQUENCES:
3 CORRESPONDENCE ADDRESS:
3 CONTATE: CA COUNTRY: USA
3 COUNTRY: USA
4 COUNTRY: USA
5 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM FC COMPALIBLE
5 COMPUTER: IBM FC COMPANIBLE
5 COMPUTER: IBM FC COMP
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,296
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                       7573-024
                                                                                         SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 822 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 822 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 VMKIADF 642
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US-08-459-296-2
i Sequence 2, Application US/08459296
i Sequence 2, Application US/08459296
i Retent No. 5670323
i GENERAL INFORMATION:
    APPLICANT: No. 5670323a, Michael
    APPLICANT: Gonzalez, Ana-Maria
    APPLICANT: Baird, Andrew
    TITLE OF INVENTION: PROCESS FOR DETECTION OF NEOPLASTIC
    TITLE OF INVENTION: DISEASE
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds
    STREET: 1155 Avenue of the Americas
    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%; Score 23; DB 1; Length 822; 57.1%; Pred. No. 1.3e+03; tive 2; Mismatches 1; Indels
                                                          Sequence 4, Application US/07921807B

Sequence 4, Application US/07921807B

Patent NO. 5474914

GENERAL INFORMATION:

APPLICANT: SPATE:

TITLE OF INVENTION: OF VIRAL PROTEINS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEB: CHIRON CORPORATION

STREET: 4560 Horton Street - R440

CITY: Emeryville

STATE: CA

COUNTRY: USA

IPP: 94608-2916

COMPUTER: Floppy disk

COMPUTER: IBP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Ploppy disk

COMPUTER: Detentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/921,807B

FILING DATE: 29-SEP-1992

CLASSIFICATION NUMBER: US/07/921,807B

FILING DATE: 29-SEP-1992

CLASSIFICATION NUMBER: US/07/921,807B

FILING DATE: 29-SEP-1992

CLASSIFICATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0209.001

TELECOMMUNICATION INFORMATION:

TELEFAX: (510) 661-2708

TELEFAX: (510) 651-2708

TENERAL: CHARACTERISTICS:

TENEVENT OF SEQUENCE SURFERSERIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 822 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 57.11
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
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                     RESULT 97
US-07-921-807B-4
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                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08451822A
| Sequence 12, Application US/08451822A
| Patent No. 5863888
| GENERAL INFORMATION:
| APPLICANT: Crumley, Greg
| APPLICANT: Crumley, Greg
| APPLICANT: Schlessinger, Joseph
| TITLE OF INVENTION: Fibroblast Growth Factor Receptors
| NUMBER OF SEQUENCES: 19
| CORRESPONDENCE ADDRESSS:
| ADDRESSEE: Rhone-Poulenc Rorer Legal Department
| STREET: 500 Arcola Road
| STREET: PA
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                                             79.3%; Score 23; DB 1; Length 822; 57.1%; Pred. No. 1.3e+03; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MAY-1995
CIASSIFICATION ATA:
APPLICATION NUMBER: US 03/33,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUJ-1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 29,699
REGISTRATION PORR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acids
TYPER: APPLICATION INPERIORED
                                             Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: peptide
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636 VMKIADF 642
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636 VMKIADF 642
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US-08-451-822A-12
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US-08-441-944A-4
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Search completed: June 13, 2005, 14:00:49

Job time : 33 secs

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GenCore version 5.1.6
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Title:	09730329-60ED
Sequence:	1 VMXVAEF 7
Scoring table: BLOSUM62	BLOSUM62
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1710399 seqs, 383334425 residues Searched:

1710399 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 300 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published_Applications_AA:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1		Sequence 80, Appl		Sequence 64091, A					Sequence 226832,	
SUMMARIES	ID	9 US-09-393-634-80	US-10-383-982-80	US-10-364-861-80	US-10-282-122A-63416	US-10-282-122A-64091	US-10-437-963-170879	US-10-282-122A-57253	US-10-425-115-187006	US-10-243-552-932	US-10-424-599-226832	US-10-013-379-11
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	Score	27	27	27	26	26	26	25	24	24	24	24
Result	No.	1	7	e	4	2	9	7	80	0	10	11

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Sequence 27 Sequence 1, Sequence 6, Sequence 7,	Sequence 8,	Sequence 70 Sequence 25	Sequence 44	Sequence 71	Sequence 14	Sequence 67	Sequence 44	Sequence 71	Sequence 44	Sequence 71	Segmence 10	Sequence 55	Sequence 18	Sequence 3,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence 12820, A	Sequence 8, Appli	Sequence 22, Appl	Sequence /1223, A	Segrence 8, Appir	Sequence 53283. A	Sequence 239771,	Sequence 7239, Ap	Sequence 153508,	Sequence 333164, A	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguenc	Sequence	Sequence	Sequence	Sequenci	Sequence	Sequence	Sequence	Sequence 1	Sequence	Sequence	comence (	Sequence 11	Seguence	Sequence 7240,	Sequence 40, A
27 1, 6,	S US-10-763-418-8 Sequence 8,	0 US-09-912-976-70 7 US-10-774-355A-2526 Seguence 25	0 US-09-510-332-44 Sequence 44	0 US-09-510-332-71 Sequence 71	4 US-10-01/-161-1934 Sequence 19 5 US-10-292-798-1478 Sequence 14	5 US-10-343-650A-672 Sequence 67	5 US-10-770-127-44 Sequence 44	5 US-10-770-127-71 Sequence 71	7 US-10-962-365-44 Sequence 44	7 US-10-962-365-71 Sequence 71	S US-10-763-418-10 Sequence 10	5 US-10-425-114-55531 Sequence 55	4 US-10-017-161-1822 Sequence 18	5 US-10-763-418-3 Sequence 3,	5 US-10-437-963-184025 Sequence	5 US-10-664-421-45 Sequence	5 US-10-282-122A-43909 Sequence	7 US-10-857-625-727 Sequence	US-09-815-242-5133 Sequence	5 US-10-282-122A-43554 Sequence	5 US-10-369-493-21613 Sequence	3 US-10-087-192-1131 Sequence	US-09-815-242-5303 Sequence	US-09-815-242-12388 Sequence	US-09-815-242-12820 Sequence 12820, A	4 US-10-138-701-8 Sequence 8, Appli	4 US-10-138-701-22 Sequence 22, Appl	5 US-IU-282-1228-/1223 Sequence /1223, A	5 US-10-823-705-0 Sequence 0, Appli	5 US-10-282-122A-53283 Sequence 53283. A	6 US-10-425-115-239771 Sequence 239771,	5 US-10-335-977-7239 Sequence 7239, Ap	5 US-10-424-599-153508 Sequence 153508,	5 US-10-425-114-43064 Sequence 3354. A	5 US-10-425-114-63937 Sequence	7 US-10-732-923-2783 Sequence	5 US-10-369-493-6182 Sequence	/ US-10-/32-923-2/82 Sequence	5 US-10-424-599-146129 Sequence	6 US-10-450-859-2 Sequence	6 US-10-437-963-131085 Sequence	5 US-10-425-114-60637 Sequence	5 US-10-425-114-45814 sequences 6 HS-10-425-115-335201 sequence	5 US-10-424-599-255268 Sequence	5 US-10-425-114-47187 Sequence	7 US-10-732-923-13660 Sequence	4 US-10-193-477-119 Sequence	7 US-10-868-5778-21 Segment	5 US-10-302-812-46 Sequence	US-09-805-020-47 Sequence	5 US-10-307-817-6 Sequence	6 US-10-437-963-134076 Sequence 1	6 US-10-425-115-239772 Sequence	7 US-10-941-486-9 Sequence 3	US-UY-YZS-3UZ-/I4 Sequence //	US-09-815-242-11330 Sequence 11	5 US-10-282-122A-58722 Sequence	s US-10-335-977-7240 Sequence 7240,	7 US-10-659-004-40 Sequence 40, A
6 US-10-664-421-27 Sequence 27 Sequence 27 Sequence 1. Sequence 1. Sequence 1. Sequence 1. Sequence 1. Sequence 7. Sequence 7.	10 16 US-10-763-418-8 Sequence 8,	12    10	14 10 US-09-510-332-44 Sequence 44	14 10 US-09-510-332-71 Sequence 71	14 14 US-IU-UI/-INI-1934 Sequence 19 14 15 US-10-292-798-1478 Sequence 14	14 15 US-10-343-650A-672 Sequence 67	14 16 US-10-770-127-44 Seguence 44	14 16 US-10-770-127-71 Sequence 71	14 17 US-10-962-365-44 Sequence 44	14 17 US-10-962-365-71 Sequence 71	19 16 US-10-763-418-10 Sequence 10	19 15 US-10-425-114-55531 Sequence 55	40 14 US-10-017-161-1822 Sequence 18	51 16 US-10-763-418-3 Seguence 3,	78 16 US-10-437-963-184025 Sequence	79 16 US-10-664-421-45 Sequence	83 15 US-10-282-122A-43909 Sequence	83 17 US-10-857-625-727 Sequence	87 9 US-09-815-242-5133 Sequence	87 15 US-10-282-122A-43554 Sequence	93 15 US-10-369-493-21613 Sequence	94 13 US-10-087-192-1131 Sequence	21 9 US-09-815-242-5303 Sequence	21 9 US-09-815-242-12388 Sequence	21 9 US-09-815-242-12820 Sequence 12820, A	21 14 US-10-138-701-8 Sequence 8, Appli	21 14 US-10-138-701-22 Sequence 22, Appl	21 15 US-10-282-122A-/1223 Sequence /1223, A	21 16 US-10-823-785-22 Semience 0, Appli	23 15 US-10-282-122A-53283 Sequence 53283. A	37 16 US-10-425-115-239771 Sequence 239771,	47 15 US-10-335-977-7239 Sequence 7239, Ap	55 15 US-10-424-599-153508 Sequence 153508,	77 15 US-10-425-114-43064 Sequence 355164, A	80 15 US-10-425-114-63937 Sequence	83 17 US-10-732-923-2783 Sequence	84 15 US-10-369-493-6182 Sequence	84 I/ US-10-/32-923-2/82 Sequence	15 15 US-10-424-599-146129 Sequence	26 16 US-10-450-859-2 Sequence	26 16 US-10-437-963-131085 Sequence	30 15 US-10-425-114-60637 Sequence	31 IS US-IU-425-II4-458I4 Sequence	81 15 US-10-424-599-255268 Sequence	97 15 US-10-425-114-47187 Sequence	12 17 US-10-732-923-13660 Sequence	50 14 US-10-193-477-119 Sequence	82 17 US-10-868-577A-21 Sequence	94 15 US-10-302-812-46 Sequence	02 9 US-09-805-020-47 Sequence	35 15 US-10-307-817-6 Sequence	35 16 US-10-437-963-134076 Sequence 1	52 16 US-10-425-115-239772 Sequence	59 I7 US-I0-94I-486-9 Sequence 3	64 y US-UY-YZS-3UZ-/I4 sequence //	73 9 US-09-815-242-11330 Sequence 11	73 15 US-10-282-122A-58722 Sequence	73 15 US-10-335-977-7240 Sequence 7240,	88 17 US-10-659-004-40 Sequence 40, A
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APPLICANT: Ryba, Nick
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APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
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APPLICANT: Mueller, Ken
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APPLICANT: Hoon, Mark
APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: S2307E-09800US
FILE REFERENCE: 02307E-0980US
CURRENT APPLICATION NUMBER: US/10/383,982
CURRENT APPLICATION NUMBER: US/03-07
PRIOR FILING DATE: 1999-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: human GR24
US-09-393-634-80
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 68
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Zuker,
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7 US-10-915-017-19
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Sequence 64091, Application US/10282122A Publication No. US20040029129A1
  APPLICATION NUMBER: 60/230,347
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ORGANISM: Mycoplasma genitalium
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71.48;
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Ohlsen, Kari
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind, Judith
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Best Local Similarity 71.4
Matches 5, Conservative
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93 VMNIAEF 99
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APPLICANT:
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: T2R, a No. US20040038312Alel Family of Taste Receptors
TITLE OF INVENTION NUMBER: US/10/364,861
CURRENT APPLICATION NUMBER: US/10/364,861
CURRENT FILING DATE: 2003-06-30
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ 1D NOS: 95
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21,078
PRIOR FILING DATE: 2000-03-21,078
PRIOR FILING DATE: 2000-05-29
PRIOR FILING DATE: 2000-05-29
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,325
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
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Pred. No. 30;
1; Mismatches 1; Indels
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                                                                                                                                                         ; Sequence 80, Application US/10364861; Publication No. US20040038312A1; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zydkind, Judith
APPLICANT: Yamick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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ORGANISM: Homo sapiens
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11 IMAVAEF 17
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11 IMAVAEF 17
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VMXVAEF 7
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US-10-364-861-80
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LENGTH: 68
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APPLICANT:
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-20-09
PRIOR PILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-18
PRIOR PRIOR PRIOR DATE: 2001-03-18
PRIOR FILING DATE: 2001-
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CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
FILE REFERENCE: ELITRA.0340
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihus
APPLICANT: Zhou, Yihus
APPLICANT: Chou, Yihus
APPLICANT: Chou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 187006
LENGTH: 118
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                                     PRIOR PAPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
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US-10-425-115-187006
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ORGANISM: Zea mays
FRATURE:
NAME/KEY: unsure
LOCATION: (1)..(118)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 187006, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Enterococcus faecalis US-10-282-122A-57253
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97 VLTIAEF 103
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APPLICANT: Wu, Wei,
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DAIE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 170879
TYPE: TAPE: TOTO
TYPE: TOTO
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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US-10-437-963-170879
                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 170879, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
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                                                                          ; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-10-282-122A-64091
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Wall, Daniel
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Matches 5; Conservative
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Carr, Grant
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ORGANISM: Oryza sativa
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93 VMNIAEF 99
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Best Local Similarity
Matches 5; Conserv
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                       SEQ ID NO 64091
LENGTH: 224
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APPLICANT:
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APPLICANT:
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Gaps

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APPLICANT: Lancaster, Laura
APPLICANT: Dallas, Anne
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
TITLE OF INVENTION: UNMBER: US/10/013,379
CURRENT APPLICATION NUMBER: US 60/254,603
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10013379
Publication No. US20020188108A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Cate, Jamie H.
APPLICANT: No. US20020188108A11er, Harry F.
APPLICANT: Yusupov, Marat M.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(134)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT3847_4685C.1.pep
US-10-424-599-226832
                                                                                                                                                                                                                                               Score 24; DB 15;
Pred. No. 3.4e+02;
1; Mismatches 1.
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Pred. No. 3.7e+02;
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OTHER INFORMATION: 50S ribosomal protein L13
OTHER INFORMATION: 191yM
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ORGANISM: Haloarcula marismortui
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APPLICANT: Baucom, Albion
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83.3%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TTTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (523.3) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 226832
LENGTH: 134
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                                                         US-10-243-552-932

sequence 932, Application US/10243552

sequence 932, Application No. US2003224379A1

centration No. US2003224379A1

sequence 932, Application No. US200324379A1

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Matches 5; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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64 LMVVAEF 70
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US-10-424-599-226832
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US-1U-199-29-20-3-40

Sequence 540, Application US/10389566

Publication No. US20040025202A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC

APPLICANT: Laurie, Cathy C

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77 (52900) D

CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT PILING DATE: 2003-03-15

PRIOR APPLICATION NUMBER: US 60/355,301

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

SOFTWARE: PatentIn version 3.2

SEQ ID NO 540

LENGTH: 195
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PRIOR DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PELION DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
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        Indels
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        2; Mismatches
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amalone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
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Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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Matches 5; Conservative
        4; Conservative
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131 LMAIAEF 137
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APPLICANT:
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PRIOR FLILING DATE: 2003-02-20

PRIOR PLICATION NUMBER: 60/191,078

PRIOR PLILING DATE: 2000-05-21

PRIOR PLILING DATE: 2000-05-23

PRIOR PLILING DATE: 2000-05-23

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-12-22

PRIOR PLILING DATE: 2001-12-22

PRIOR PLILING DATE: 2001-02-26

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-01

PRIOR PLING DATE: 2001-02-01
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                        Score 24; DB 15; Length 180;
Pred. No. 4.7e+02;
0; Mismatches 1; Indels
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US-10-424-599-170244
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 170244
LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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57.1%;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 83.3
Matches 5; Conservative
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Trawick, John
                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
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US-10-282-122A-52538
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LENGTH: 191
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 54190
LENGTH: 238
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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72 VLSIAEF 78
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PALICATION NUMBER: 60/201, 078

PRIOR APPLICATION NUMBER: 60/201, 078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/206, 848

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR APPLICATION NUMBER: 60/206

PRIOR APPLICATION NUMBER: 60/206

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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US-10-282-122A-54190
Sequence 54190, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Ollsen, Kari
APPLICANT: Yskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Garr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Fawick, Sobert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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131 LMAIAEF 137
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LENGTH: 195
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Sequence 1738, Application US/10472928

Sequence 1738, Application No. US2050020813A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS

TITLE OF INVENTION STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS

CURRENT APPLICATION NUMBER: US/10/472,928

CURRENT APPLICATION NUMBER: 08-10.0568.7

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4979

SEQ ID NO 1738

LENGTH: 335
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.0348
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 6-phosphofructokinase (pfk)

OTHER INFORMATION: Cellular location: cytoplasm

OTHER INFORMATION: Similar to strain R6 sequence 15902840 (0.E+01)
US-10-472-928-1738
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     Indels
     5
     Mismatches
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US-10-282-122A-51530
; Sequence 51530, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Andlone, Carlos
; APPLICANT: Andlone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Oykind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Mall, Daniel
; APPLICANT: Mall, Daniel
; APPLICANT: Gyskind, Judith
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PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptococcus pneumoniae
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Yamamoto, Robert
Forsyth, R.
     5; Conservative
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                                                                                                                  224 VMSAAEF 230
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Best Local Similarity
                                                             1 VMXVAEF 7
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APPLICANT:
APPLICANT:
     Matches
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Publication No. US20040110181A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
TITLE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOUTWARE: Patentin version 3.1
SEQ ID NO 654
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/202
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR PLILING DATE: 2000-110-20
PRIOR FILING DATE: 2000-110-20
PRIOR PRILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PLILNG DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73914
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                                                                                                                                         Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                daselbeck, Robert
                                                                                 Zyskind, Judith
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Matches 5; Conservative
     Malone, Cheryl
                                                       Ohlsen, Kari
                                                                                                                  Daniel
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Best Local Similarity
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LENGTH: 335
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US-10-474-776-654
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APPLICANT
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US-10-739-930-5878
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Sequence 5878, Application US/10739930

Sequence 5878, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE FERENCE: 38-21(5337)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

SEQ ID NOS: 11088

LENGTH: 378
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PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PLING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-02

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

SPRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

SPRIOR SPECIAL APPLICATION NUMBER: 60/269,308

PRIOR SPECIAL APPLICATION NUMBER: 60/269,308

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; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT EdgeTCON, Michael D
; TITLE OF INVENTION: TANAGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796) C
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14226
; LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-732-923-14226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Arabidopsis thaliana
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RESULT 24

US-10-081-816-14

US-10-083-816-14

Sequence 14, Application US/10081816

Publication No. US20030045472A1

GENERAL INFORMATION:

APPLICANT: ARE1, Richard

APPLICANT: Scott, Kristin

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 0575/64019-A/JFW/ADM

CURRENT APPLICATION NUMBER: US/10/081,816

CURRENT APPLICATION NUMBER: 60/271,319

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 14

SEQ ID NO 14

LENGTH: 409
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US-10-437-963-131765

US-10-437-963-131765

Sequence 131765, Application US/10437963

Sequence 131765, Application No. US20040123343A1

SEQUENCE 131765

SEQUENCE 131765

APPLICANT: Brosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cac, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

SEQ ID NOS: 204966

SEQ ID NOS: 204966

SEQ ID NOS: 204966
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Score 24; DB 16; Length 378;
Pred. No. 1e+03;
1; Mismatches 1; Indels
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US-10-437-963-131765
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Pred. No. 1.1e+03;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.49
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                        | | : | | |
48 VMNMAEF 54
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                                                                                              1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 46068
LENGTH: 902
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                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION WHBEE: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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83.3%; Pred. No. 2.2e+03;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 142919, Application US/10437963
PUblication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Show, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                     ; Sequence 46060, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-03-35
PRIOR PILING DATE: 2000-03-66
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46060
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Forsyth, R.
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Best Local Similarity 83.3
Matches 5; Conservative
                            || |||:
94 VMLVAEY 100
1 VMXVAEF 7
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                                                                                                                      RESULT 26
US-10-282-122A-46060
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LENGTH: 807
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/242,578

PRIOR PLICATION NUMBER: 60/242,578

PRIOR PLICATION NUMBER: 60/242,578

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/257,931

PRIOR PLILING DATE: 2000-11-22

PRIOR PLILING DATE: 2001-12-22

PRIOR PLILING DATE: 2001-12-22

PRIOR PLILING DATE: 2001-12-22

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-06

PRIOR PLILING DATE: 2001-02-06
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_43879C.1.pep
US-10-437-963-142919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46068, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: ABelbeck, Robert
APPLICANT: ABelbeck, Robert
APPLICANT: Zyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yersyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.8
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :|:|
206 VMTIADF 212
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acis	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	
PRT ISM: Bacillus anthracis	YKEY: MISC FEATURE TION: (30)(30)	KEY: MISC FEATURE ION: (215)	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (222)(222) OTHER INFORMATION: X=any	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (543)(543) OTHER INFORMATION: X=any	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (549)(549) OTHER INFORMATION: X=any	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (556)(556) OTHER INFORMATION: X=any		FEATURE: NAME/KEY: MISC FEATURE LOCATION: (597)(597) OTHER INFORMATION: X=any	KEY: MISC FEATURE ION: (635)(635) INFORMATION: X=any	RE: KEY: MISC_FEATURE ION: (649)(649) :INFORMATION: X=any	RE: KEY: MISC_FEATURE ION: (659) INFORMATION: X=any	KEY: MISC FEATURE ION: (663)(663) INFORMATION: X-any	RE: KEY: MISC_FEATURE ION: (687)(687) INFORMATION: X=any	KEY: MISC FEATURE ITON: (693)(693)	KEY: MISC FEATURE ION: (711)(711)	KEY: MISC FEATURE ION: (718)(718) INFORMATION: X=any	KEY: MISC FEATURE ION: (732)(732)	KEY: MISC FEATURE ION: (737)(737)
TYPE: PRT ORGANISM:	NAME/KEY: LOCATION: OTHER INF	FEATURE: NAME/KEY: LOCATION: OTHER INFO	FEATURE: NAME/KEY LOCATION OTHER IN	FEATURE: NAME/KEY LOCATION OTHER IN	realore: NAME/KEY LOCATION OTHER IN	FEATURE: NAME/KEY LOCATION OTHER IN	FEATURE: NAME/KEY LOCATION OTHER IN	FEATURE: NAME/KEY LOCATION OTHER IN	FEATURE: NAME/KEY: LOCATION: OTHER INFC	FEATURE: NAME/KEY: LOCATION: OTHER INFC	FEATURE: NAME/KEY: LOCATION: OTHER INFO	FEATURE: NAME/KEY: LOCATION: OTHER INFC	FEATURE: NAME/KEY: LOCATION: OTHER INFO	FEATURE: NAME/KEY: LOCATION: OTHER INFO	FEATURE: NAME/KEY: LOCATION: OTHER INFO	FEATORE: NAME/KEY: LOCATION: OTHER INF	FEATURE: NAME/KEY: LOCATION: OTHER INF	realore: NAME/KEY: LOCATION:
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RESULT 29
10-160-493-5367
1 Sequence 5367, Application US/10369493
1 Sequence 5367, Application US/10369493
1 Sequence 5367, Application No. US20030233675A1
1 GENERAL INPORMATION:
2 APPLICANT: Cao, Yongwei
3 APPLICANT: Stater, Steven C.
3 APPLICANT: Stater, Steven C.
4 APPLICANT: Chen, Xianfeng
5 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
2 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
3 FILE REFERENCE: 38-10(52052) B
4 CURRENT APPLICATION NUMBER: US/10/369,493
5 CURRENT APPLICATION NUMBER: US/60/360,039
6 PRIOR FILING DATE: 2002-02-28
6 PRIOR FILING DATE: 2002-02-28
6 NUMBER OF SEQ ID NOS: 47374
6 SEQ ID NO 5367
6 LENGTH: 919 ö RESULT 30
US-10-282-122A-70737
i Sequence 70737, Application US/10282122A
j Publication No. US20040029129A1
j GENERAL INPORMATION:
APPLICANT: Wang, Liangsu
j APPLICANT: Malone, Carly
APPLICANT: Haselbeck, Robert
APPLICANT: APPLICANT: Xyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: FORSYth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A ö Gaps Gaps . 0 ö Length 902; Query Match
82.8%; Score 24; DB 15; Length 919;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Indels Query Match 82.8%; Score 24; DB 15; Best Local Similarity 83.3%; Pred. No. 2.5e+03; Matches 5; Conservative 0; Mismatches 1; PEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (809)...(809)

OTHER INFORMATION: X=any amino acid
FEATURE:

NAME/KEY: MISC FEATURE

NAME/KEY: MISC FEATURE

LOCATION: (810)...(810)

OTHER INFORMATION: X=any amino acid

US-10-282-122A-46068 TYPE: PRT; ORGANISM: Caenorhabditis elegans US-10-369-493-5367 || |||: 592 VMIVAEY 598 113 MTVAEF 118 1 VMXVAEF 7 2 MXVAEF 7 임 g ò ò

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Sequence 73, Application US/10154419

Sequence 73, Application US/10154419

Publication No. US20030143675A1

GENERAL INFORMATION:

APPLICANT: CUtatis, Rory A.J.

APPLICANT: Glucksman, Maria Alexandra

APPLICANT: Glucksman, Maria Alexandra

APPLICANT: Glucksman, Maria Alexandra

APPLICANT: Glucksman, Maria Alexandra

TITLE OF INVENTION: 87259, 6718, 67067, 62099, 46455, 84414, 53763,

TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THEREFOR

TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THEREFOR

TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THEREFOR

TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THEREFOR

TITLE OF INVENTION: AND 5725A1 MOLECULES AND USES THEREFOR

TITLE OF INVENTION OF THE TOWN OF T
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; Sequence 23, Application US/10024623
; Publication No. US2020187524A1
; GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
TITLE OF INVENTION: USE THEREOF
; TITLE OF INVENTION: 0508 THEREOF
; TITLE OF INVENTION: USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT TILING DATE: 2000-12-15
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 23
; LENGTH DATE: PASISED for Windows Version 4.0
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82.8%; Score 24; DB 14; Length 1084;
Best Local Similarity 71.4%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels (
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                                                                1; Indels
          Pred. No. 2.7e+03;
1; Mismatches 1
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Pred. No. 3e+03
1; Mismatches
          71.48;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                5, Conservative
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CRGANISM: Homo sapiens
US-10-024-623-23
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1016 LMVVAEF 1022
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                 1 VMXVAEF 7
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Sequence 24, Application US/10100049

Publication Wo. US20030078398A1

GENERAL INFORMATION:
APPLICANT: Graham, Margaret
APPLICANT: Graham, Margaret
APPLICANT: Munn, Edward
APPLICANT: Munn, Edward
APPLICANT: Oliver, Joanna
APPLICANT: Oliver, Joanna
APPLICANT: Newton, Susan
APPLICANT: Oliver, Joanna
APPLICANT: Newton, Susan
APPLICATION NUMBER: US 09/129366
APRIOR FILING DATE: 1998-08-05
APRIOR PILING DATE: 1998-06-05
APRIOR FILING DATE: 1993-05-07
APRIOR PILING DATE: 1992-05-07
APRIOR PILING DATE: 1992-05-07
APRIOR PILING DATE: 1992-05-06-08
APRIOR PILING DATE: 1992-05-06
APPLICANT: NUMBER OF SEC 1D NOS: 75
APPLICANT: NUMBER OF SEC 1D NOS: 75
APPLICANT: NUMBER OF SEC 1D NOS: 75
APPLICANT: NOTE APPLICANT NUMBER: US NUMBER OF SEC 1D NOS: 75
APPLICANT: 
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                          PRIOR FILING DATE: 2003-02-20
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-03-21
FRIOR PLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR PILING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/242,578
FRIOR APPLICATION NUMBER: 60/242,578
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR PILING DATE: 2000-10-23
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR PLING DATE: 2001-02-09
FRIOR PLING DATE: 2001-02-09
FRIOR PLING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PLING DATE: 2001-02-06
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PLING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PLING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR PLING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/260,308
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Pred. No. 2.5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Haemonchus contortus
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Best Local Similarity 83.3
Matches 5; Conservative
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82.8%; Score 24; DB 14; Length 972;

Query Match

1016 LMVVAEF 1022

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Pred. No. 3e+03;
1; Mismatches 1; Indels
Sequence 68, Application US/10146733
Publication No. US20030165891A1
                                                                                                                                                                                                                                                                       82.8%;
                                                                                                                                                                                                                                                                       Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapiens
US-10-146-733-68
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1016 LMVVAEF 1022
                                                                                                                                                                                                                                                                                        1 VMXVAEF 7
        GENERAL INFORMATION:
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Sequence 26, Application US/10024623

Sequence 26, Application US/10024623

Publication No. US20020187524A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.:

TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: 0508 THEREOF

TITLE OF INVENTION: 0708 THEREOF

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                               82.8%; Score 24; DB 13; Length 1095; 71.4%; Pred. No. 3e+03; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
COCATION: 801, 1005
COTHER PROGRAPTION: Xaa = any amino acid
US-10.024-623-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-623-26
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Best Local Similarity
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RESULT 35
US-10-024-623-26
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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ORGANISM: Homo sapiens
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1016 LMVVAEF 1022
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                                                                                            APPLICANT: Cuttis, Rory A.J.
APPLICANT: Cuttis, Rory A.J.
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,
TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FBH58295FL, 57255,
FILE REFERENCE: MNI-249
CURRENT APPLICATION NUMBER: US/10/154,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CURTIES, Rory A.J.
APPLICANT: CURTIES, Rory A.J.
APPLICANT: Gluckeman, Maria Alexandra
TITLE OF INVENTION: 87259, 67118, 67064, 6109, 46455, 54414, 53763,
TITLE OF INVENTION: 67076, 671102, 44181, 67084ALT, PBH58295FL, 57255,
TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
TITLE OF INVENTION: 401055alt MOLECULES AND USES THEREFOR
FILE REPERBNCE: MN1-29
CURRENT APPLICATION NUMBER: US/10/154,419
CURRENT FILING DATE: 2002-05-22
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ Version 4.0
SEQ ID NO 86
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Pred. No. 3e+03;
1; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                               Prior. vo/10/154,419
Prior. Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 801, 1005
; OTHER INFORMATION: Xaa = any amino acid
US-10-154-419-86
                                                      ; Sequence 76, Application US/10154419; Publication No. US20030143675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 86, Application US/10154419; Publication No. US20030143675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     82.8%;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-419-76
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1016 LMVVAEF 1022
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                            LENGTH: 1095
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US-10-154-419-86
                                         10-154-419-76
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RESULT 40 US-10-146-733-81 ; Sequence 81, Application US/10146733

RESULT 39

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FILE REPERENCE: ELITRA, 034A

CURRENT APPLICATION: IGENILITICATION OF ESBENLIAIL GENES IN MICROLOGIMENT FILE REPERENCE: ELITRA, 034A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PLICATION NUMBER: 60/207, 727

PRIOR PLICATION NUMBER: 60/207, 727

PRIOR PLICATION NUMBER: 60/207, 727

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-2-20

PRIOR PLING DATE: 2001-12-2-69

PRIOR PLING DATE: 2001-02-16

PRIOR PRIOR PLING DATE: 2001-02-16

PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24; DB 15; Length 1225;
Pred. No. 3.4e+03;
1; Mismatches 1; Indels
           Sequence 56058, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Enterobacter cloacae US-10-282-122A-56058
                                                                                                                                                    Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%;
                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
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US-10-437-963-200466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 801, 1005
; OTHER INFORMATION: Xaa = any amino acid
US-10-146-733-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.8%;
71.4%;
Publication No. US20030165891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
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APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement Sequence 200666, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad

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Gaps

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RESULT 41

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Gaps
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US-09-158-722-47

Sequence 47, Application US/09158722

Sequence 47, Application WS/09158722

Publication No. US20030013848A1

GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg B.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: La Jolla

CITY: La Jolla
                                                                                                                                                                                                      TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 10;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-0MN-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                    US-09-158-722-46
; Sequence 46, Application US/09158722
; Publication No. US20030013848A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | :|:|
9 VMKIADF 15
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                                                                                                                                                                                                                                                                           Score 24; DB 16; Length 2059;
Pred. No. 5.8e+03;
2; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-158-722-18
Sequence 18, Application US/09158722
Sequence 18, Application US/09158722
Sublication No. US20030013848A1
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: La Jolla
                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_95932C.1.pep
US-10-437-963-200466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/158,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-JUM-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
FILING DATE: 10-MAY-1992
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAM: (619) 678-5070
TELEFAM: (619) 678-5070
TELEFAM: CAMPARCTERISTICS:
SEQUENCE CHARACTERISTICS:
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 200466
LENGTH: 2059
                                                                                                                                                                                                                                                                             82.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 amino acids
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-09-158-722-18
                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                 :: ||||
1869 ILAVAEF 1875
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1 VMXVAEF 7

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WS-09-864-408A-40
| Sequence 40, Application US/09864408A
| Sequence 40, Application No. US20040009474A1
| PUBLication No. US20040009474A1
| GENERAL INFORMATION:
| APPLICANT: Leach, Martin D. APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: SOUNCE: 21402-012
| CURRENT APPLICATION NUMBER: US/09/864,408A | CURRENT APPLICATION NUMBER: 00/206,690 | PRIOR PILING DATE: 2000-05-24 | NUMBER OF SEQ ID NOS: 9068 | SOFTWARE: PastSEQ for Windows Version 4.0 | SEQ ID NO 40 | SEQ 
                                                                                                                                                          Wis-10-767-701-50646

Sequence 50646, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: APPLICANT: And Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement TITLE OF INVENTION: WUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 50646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3480-021-P1-K1-H3.pep
US-10-767-701-50646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 16;
Pred. No. 2.8e+02;
0; Mismatches 2
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APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Sorghum bicolor
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CRGANISM: Homo sapiens
US-09-864-408A-40
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| :|||
14 MTIAEF 19
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US-09-393-634-76
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 169354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23, DB 15; Length 61;
Pred. No. 2.7e+02;
1; Mismatches 1; Indels
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US-10-424-599-169354
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION UMBER: US/09/158,722
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        FILING MARE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-UNA-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
NAME: Wetherell Ph.D., John R.
REFERENCE/DOCKET NUMBER: 07251/007002
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION OF 78-5099
INFORMATION FOR SEQ ID NO. 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-722-47
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ORGANISM: Glycine max
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9 VMKIADF 15
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                               COUNTRY: U
ZIP: 92037
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2 MXVAEF 7

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Application US/10383982
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11 ILAIAEF 17
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NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-383-982-76
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| Sequence 40, Application US/09510332
| Sequence 40, Application US/09510332
| Sequence 40, Application No. US20030022278A1
| Sequence 40, Application No. US20030022278A1
| Septicant: Adler, Jon Elliot
| APPLICANT: Adler, Jon Elliot
| APPLICANT: Mueller, Ken
| APPLICANT: Hoon, Mark
| APPLICANT: Hoon, Mark
| APPLICANT: Hoon, Mark
| Septicant: Hoon, Mark
| APPLICANT: Hoon, Mark
| APPLICANT: Hoon, Mark
| Septicant: Hoon Willian Of Taste Receptors
| TITLE OF INVENTION: T2R, a No. US20030022278A1el Family of Taste Receptors
| TITLE OF INVENTION: UNMBER: US 030/59/510, 332
| CURRENT APPLICATION NUMBER: US 09/393,634
| PRIOR FILING DATE: 1999-09-10
| NUMBER OF SEQ ID NOS: 172
| SOFTWARE: PatentIn Ver. 2.1
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                    APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SP, a No. US20020051997A1e1 Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 23; DB 9; Length 90; 42.9%; Pred. No. 4.1e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
CTHER INFORMATION: human GR22
NAME/KES: MOD. RES
LOCATION: (1)..(90)
CTHER INFORMATION: Xaa = any amino acid
US-09-393-634-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(90)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: human T2R22 (hGR22)
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                      Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.3
Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
  Mueller, Ken
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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                                                                                                                                                                                                                                                                                        SEQ ID NO 76
LENGTH: 90
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LENGTH: 90
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RESULT 51 US-10-383-982-76

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Sequence 76, Application US/10364861

Sequence 76, Application US/10364861

Publication No. US20040038312A1

GENERAL INFORMATION:

APPLICANT: Calver, Charles S.

APPLICANT: Application Nor Elliot

APPLICANT: Ryba, Nick

APPLICANT: The Regents of the University of California

APPLICANT: The Regents of the University of the APPLICANT: The Government of the United States of America

APPLICANT: The Government of Health and Human Services

TILEO OF INVENTION: TSR, a No. US20040038312A1e1 Family of Taste Receptors

FILE REFERENCE: 02307E-098020US

CURRENT APPLICATION NUMBER: US/10/364,861

CURRENT APPLICATION NUMBER: US 09/393,634

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 76

LENGTH: 90

TANDER DATE: CALVER DATE: CALVE DA
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                                                                                                                                                                                                                                                                                                         APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California APPLICANT: The Government of the United States of America APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary of the APPLICANT: as represented by the Secretary of the Secretary of the Separation of Health and Human Services TITLE OF INVENTION: SF, a No. US20030157568A1e1 Family of Taste Receptors FILE REFERENCE: 023078-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1990-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 76
LENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 14;
42.9%; Pred. No. 4.1e+02;
tive 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(90)
OTHER INFORMATION: human GR22
OTHER INFORMATION: Xaa = any amino acid
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; OTHER INFORMATION: Xaa = any amino acid
US-10-364-861-76
. US20030157568A1
                                                                                  APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
Mueller, Ken
APPLICANT: Mueller, Ken
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Best Local Similarity 42.5
Bernand 3; Conservative
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ORGANISM: Homo sapiens
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RESULT 56
US-10-385-415-119
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| Publication No. US20040214239A1
| GENERAL INFORMATION:
| APPLICANT: SERVANT, GUY
| APPLICANT: SERVANT, GUY
| APPLICANT: BRUST, PAUL
| APPLICANT: XU, HONG
| TITLE OF INVENTION: FUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEINS
| TITLE OF INVENTION: AND T2R MODULATORS
| TITLE OF INVENTION: AND T2R MODULATORS
| TITLE OF INVENTION: AND T2R MODULATORS
| FILE REFERENCE: 100337.54281US
| CURRENT APPLICATION NUMBER: US/10/770,127
| CURRENT APPLICATION NUMBER: 60/44,172
| PRIOR APPLICATION NUMBER: 60/44,172
| PRIOR APPLICATION NUMBER: 60/457,318
| PRIOR FILING DATE: 2003-03-26
| NUMBER OF SEQ ID NOS: 210
| SOFTWARE: PATENT OF SEQ ID NOS: 210
| SEQ ID NO 40
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; Publication No. US20050048586A1
; GENERAL INFORMATION:
; APPLICANT: Zuker; Charles S.
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: Hoon, Mark
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: T2X, a Novel Family of Taste Receptors
; FILE REFERENCE: 02307E-098010US
; CURRENT APPLICATION NUMBER: US/10/962,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%; Score 23; DB 16; Length 90; 42.9%; Pred. No. 4.1e+02; ive 3; Mismatches 1; Indels
79.3%; Score 23; DB 15; Length 90; 42.9%; Pred. No. 4.1e+02;
                                             1; Indels
                                             3; Mismatches
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LOCATION: (35)..(35)
OTHER INFORMATION: Variable amino acid
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LOCATION: (397..(39)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (82); OTHER INFORMATION: Variable amino acid US-10-770-127-40
                     Local Similarity 42.9
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11 ILAIAEF 17
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ILAIAEF 17
                                                                                          1 VMXVAEF 7
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Best Local Similarity
Matches 3; Conserv
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US-10-770-127-40
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US-10-962-365-40
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  Query Match
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Matches
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Sequence 119, Application US/10385415

Formal District Construction No. US20040014158A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bacher, Adalbert
APPLICANT: Bricher, Markus
TITLE OF INVENTION: PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAINING
TITLE OF INVENTION: A CERTAIN QUANTITIY OF SAID PROTEIN CONJUGATES
FILE REFERENCE: 9286.6CT
CURRENT APPLICATION NUMBER: US110/385,415
CURRENT PILING DATE: 2003-03-10
PRIOR FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Show Yihua
APPLICANT: Cano Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53223)8
CURRENT FILIAGO DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173522
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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US-10-424-599-173522
                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 23; DB 17; 42.9%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 15;
Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: US/09/510,332
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION WUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ 1D NOS: 172
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 40
TYPE: PRT
ORGANIEM: HOMO SADIENS
PRATURE: NAME/KEY: MOD_RES
LOCATION: (1)...(90)
CUTHER INFORMATION: human T2R22 (hGR22)
CUTHER INFORMATION: Xaa = any amino acid
US-10-962-365-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-173522
; Sequence 173522, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 42.5.
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11 ILAIAEF 17
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Garegory J.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: VONDER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION OF SEQ ID NOS: 47374
SEQ ID NO 18481
       Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Lactococcus lactis
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Matches 5; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 :|||
37 MTIAEF 42
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US-10-424-599-231564
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                                                                                                                                                                                                                                                                                                          Score 23; DB 15; Length 143;
Pred. No. 6.6e+02;
0; Mismatches 1; Indels
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APPLICANT: Oblean, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Tradic Judith W.
APPLICANT: Tradic Judith W.
APPLICANT: Tradic Judith W.
APPLICANT: Tradic Judith D.
APPLICANT: Tradic Judith D.
APPLICANT: Tradic Judith D.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR FILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
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PRIOR APPLICATION NUMBER: PCT/EP00/01899
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: DE 19910102.7
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 119
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4899, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                  ORGANISM: Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Enterococcus faecalis
US-09-815-242-4899
                                                                                                                                                                                                                                                                                                               79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Then 5; Conservative
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Matches 4; Conservative
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LMDIAEF 46
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US-10-369-493-18481
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US-09-815-242-4899
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LENGTH: 150
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APPLICANT: LA KOVALICA, Thomas J.
APPLICANT: LA KOVALICA, Thomas J.
APPLICANT: La KOVALICA, David K.
APPLICANT: Tobu, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Browkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERRNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
KUMBER OF SEQ ID NOS: 204966
SEQ ID NO 184028
LENGTH: 173
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                                                       Gaps
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79.3%; Score 23; DB 15; Length 162; 66.7%; Pred. No. 7.5e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_81060C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                           Sequence 184028, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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Sequence 18481, Application US/10369493

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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoro, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE REFRENCE: ELITRA.0348
TITLE REFRENCE: ELITRA.0340.220
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-6/23

PRIOR FILING DATE: 2000-05-6/6

PRIOR PILING DATE: 2000-05-6/6

PRIOR PILING DATE: 2000-05-9/6

PRIOR PILING DATE: 2000-05-9/6

PRIOR PILING DATE: 2000-05-9/6

PRIOR PILING DATE: 2000-05-0/3

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-2/2

PRIOR PILING DATE: 2001-02-6/6

PRIOR FILING DATE: 2001-02-6/6

PRIOR FILING DATE: 2001-02-6/6

PRIOR PILING DATE: 2001-02-6/6

PRIOR FILING DATE: 2001-02-6/6
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Pred. No. 8.8e+02;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Applicant: Oblesn, Kari
APPLICANT: Oblesn, Kari
APPLICANT: Oblesn, Kari
APPLICANT: Oblesn, Mari
APPLICANT: Mall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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US-10-282-122A-77681
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APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(3)223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 231564

LENGTH: 177

TYPP:
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Publication No. US20030148324A1
GENERAL INFORMATION:
Publication No. US20030148324A1
GENERAL INFORMATION:
Publication No. US20030148324A1
GENERAL INFORMATION:
PUBLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
FILE REFE
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Pred. No. 8.7e+02;
2; Mismatches 1; Indels
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Malone, Carlos
; APPLICANT: Malone, Chery1
; APPLICANT: Malone, Chery1
; APPLICANT: Ohlsen, Kari
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Zyskind, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%;
57.1%;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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; ORGANISM: Escherichia coli
US-10-238-075-1037
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Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
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84 MMLIAEF 90
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US-10-238-075-1037
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 0123535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 237
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Sequence 182, Application US/10334143

Sequence 182, Application US/10334143

GENERAL INFORMATION:

APPLICANT: GRIGORIEV. IGOR VYACHESLAVOVICH

APPLICANT: GRIGORIEV. IGOR VYACHESLAVOVICH

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

FILE REFERENCE: 038602/1543

CURRENT APPLICATION NUMBER: US/10/334,143

CURRENT FILING DATE: 2002-12-31

PRIOR APPLICATION NUMBER: 60/343,169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 16; Length 237; 85.7%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILLE OF INVENTION: No. US20030236392Alel full length cDNA FILE REPERRICE: HI-40105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT APPLICATION NUMBER: US/25
PRIOR APPLICATION NUMBER: NUMBER: NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 2422
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Clone ID: SORBI-28MAY03-C120919_1.pep
US-10-767-701-36898
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(237)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20030236392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.77
Thes 6; Conservative
                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-2492
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US-10-104-047-2492
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PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PLING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 78614

NUMBER OF SEQ ID NOS: 78614

SEQ ID NO 72561

LENGTH: 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAYSHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR PAPLICATION NUMBER: JP 99/377484
PRIOR PLILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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; Publication No. US20040172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4458, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOSUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptococcus mutans
US-10-282-122A-72561
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 IISVAEF 70
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74 ILSIAEF 80
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US-10-767-701-36898
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APPLICANT:
APPLICANT:
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Page 24

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1 VMXVAEF 7
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  26 MLVAEF 31
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US-09-738-626-4505
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                                                                                                                                                                         ; OTHER INFORMATION: Description of Unknown Organism: 1fgkA protein sequence US-10-334-143-182
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence | 15615, Application US/10732923
| Publication No. US20050108791A1
| GENERAL INFORMATION:
| APPLICANT: Edgerform, Michael D
| TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
| FILE REPERENCE: 38-15(52796)C
| CURRENT FILING DATE: US/10/732,923
| CURRENT FILING DATE: 2003-12-10
| PRIOR APPLICATION NUMBER: 10/310,154
| RIOR FILING DATE: 2003-12-04
| NUMBER OF SEQ ID NOS: 24149
| SEQ ID NO 15615
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 15746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 23; DB 17; Length 249; 83.3%; Pred. No. 1.2e+03; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                          79.3%; Score 23; DB 15; Length 245; 57.1%; Pred. No. 1.1e+03; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-732-923-15746
Sequence 15746, Application US/10732923
Sequence 15746, Application US/10732923
General INFORMATION:
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PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 182
LENGTH: 245
                                                                                                       TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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ORGANISM: Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                        || :|:|
131 VMKIADF 137
                                                                                                                                                                                                                                                                                                                                   1 VMXVAEF 7
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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2 MXVAEF 7

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Sequence 42888 Application US/10767701

Sequence 42888 Application US/10767701

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROOT STAND:
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
LENGTH 261

LENGTH 265

LENGTH 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C29394_1.pep
US-10-767-701-42888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3%; Score 23; DB 16; Best Local Similarity 57.1%; Pred. No. 1.2e+03; Matches 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WS-10-470-957-23

Sequence 23, Application US/10470957

PUBLICATION NO. US20040142404A1

GENERAL INPORMATION:
APPLICANT: Wilk, Andrew Frederick
APPLICANT: Wilk, Andrew Frederick
APPLICANT: Atkin, Julie
TITLE OF INVENTION: Protein kinase signalling
FILE REFERENCE: 529282001000
CURRENT APPLICATION NUMBER: US/10/470,957

CURRENT APPLICATION NUMBER: PR 2791

PRIOR FILING DATE: 2002-01-30

PRIOR FILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 51

SEQ ID NO 23

LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :|:|
150 VMKIADF 156
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APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: HIRTH, MICHAEL VANCE
ITITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REPERENCE: 0393-63/0303
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-01-02
PRIOR PILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Unknown Organism: FGFR1 tyrosine kinase; OTHER INFORMATION: sequence
US-10-377-268-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 16;
Pred. No. 1.4e+03;
2; Mismatches 1
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PELICATION NUMBER: US/10/282,122A

PRIOR PELING DATE: 2003-02-20

PRIOR PELING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-28

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-66

PRIOR PELING DATE: 2000-05-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2000-12-22
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Sequence 52955, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malnow, Cheryl
APPLICANT: Malnow, Cheryl
APPLICANT: Applicant: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Yaskind, Judith
APPLICANT: Tynkind, Judith
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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165 VMKIADF 171
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APPLICANT:
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US-10-424-599-147161
Sequence 147161, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 2003-04-28
; CURRENT APPLICATION UNMER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 9; Length 280; 71.4%; Pred. No. 1.3e+03; ive 1; Mismatches 1; Indels
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US-10-424-599-147161
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-4505
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US-10-377-268-29
; Sequence 29, Application US/10377268
; Publication No. US20040171062A1
                     MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: ||||
VVVVAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
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LENGTH: 287
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LENGTH: 280
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                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 78
US-10-763-418-31
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US-10-470-957-21
                                                                                                      US-10-763-418-13
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Publication No. US20040185547A1

GENERAL INFORMATION:
APPLICANT: MCHAMMADI MOOSA

APPLICANT: MCHAMMADI MOOSA

TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT FILING DATE: 2004-01-26

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/10/763,418

PRIOR APPLICATION NUMBER: 09/188,809

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 41

NUMBER OF SEQ ID NOS: 41
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US-10-334-143-203
; Sequence 203, Application US/10334143
; Sequence 203, Application US/10334143
; GENERAL INFORMATION:
; APPLICANT: GRICGRIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENITON: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENITON: KINASES IDENTIFIED WITH THE METHOD
; FILE REPREBRENCE: 038602/1543
; CURRENT APPLICATION NUMBER: 60/343,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                             Gaps
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remalning Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
ERQ ID NO 52955
LENGTH: 293
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                                                                                                                                                                                                                               ; ORGANISM: Clostridium difficile US-10-282-122A-52955
                                                                                                                                                                                                                                                                                                       Query Match 79.3
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-334-143-203
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173 VMKIADF 179
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LENGTH: 299
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Sequence 31, Application US/10763418

Sequence 31, Application US/10763418

Sequence 31, Application No. US20040185547A1

GENERAL INFORMATION:
APPLICANT: MCHAWADI, MOOSA

APPLICANT: MCHAWADI, MOOSA

APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPPOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPPOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPPOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: UNBER: US/10/763,418

CURRENT FILING DATE: 2000-09-18

PRIOR FILING DATE: 1998-11-09

PRIOR PRILOR APPLICATION NUMBER: 09/101,191

PRIOR PLILNG DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 31

LENGTH DATE

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Pred. No. 1.4e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                         Length 299;
                                                                                                                                                                                                                                                79.3%; Score 23; DB 16; Length 29
57.1%; Pred. No. 1.4e+03;
tive 2; Mismatches 1; Indels
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Sequence 21, Application US/10470957
Publication No. US200401424041
GENERAL INFORMATION:
APPLICANT: Cytopia Pty Ltd
APPLICANT: Wilks, Andrew Frederick
APPLICANT: Arkin, Julie
APPLICANT: Arkin, Julie
TITLE OF INVENTION: Forchin kinase signalling
FILE PEFERENCE: 5222201000
CURRENT FILING DATE: 2003-07-30
CURRENT FILING DATE: 2003-07-30
FRIOR FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/AU02/00088
PRIOR PRILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
LENGHIS DRI
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Best Local Similarity 57.1%;
Matches 4; Conservative ;
                                                                                                                                                                                                                                                     Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
SEQ ID NO 13
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
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172 VMKIADF 178
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172 VMKIADF 178
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                                                                                                                                                                                                                                                                                                                   APPLICANT: WICKERSHAM JOHN A.
APPLICANT: WICKERSHAM JOHN A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GEBRING, MICHAEL R.
APPLICANT: KAN, CHEN-CHEN
APPLICANT: KANSSTOF
TITLE OF INVENTION: MODIFICATION SOF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: MODIFICATION OF USE
FILE REFERENCE: 0125-0016US
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/330,326
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN OF: 2.0
SSOFTWARE: PATENTIN OF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WICKERSHAW, JOHN A.
APPLICANT: WICKERSHAW, JOHN A.
APPLICANT: SHOWGALTER, RICHARD
APPLICANT: SHOWGALTER, RICHARD
APPLICANT: SHOWGALTER, RICHARD
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GERRING, MICHAEL R.
APPLICANT: GERRING, MICHAEL R.
APPLICANT: WILLAFRANCA, J. ERNEST
APPLICANT: VILLAFRANCA, J. ERNEST
APPLICANT: VILLAFRANCA, J. ERNEST
APPLICANT: WAN CHEN-CHEN
APPLICANT: WAN CHEN-CHEN
APPLICANT: WAN CHEN-CHEN
APPLICANT: WODIFFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 0.125-001608
CURRENT APPLICATION NUMBER: 09/390,326
PRIOR FILING DATE: 199-90-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEV. 2.0
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                            Gaps
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                          1; Indels
Pred. No. 1.5e+03;
2; Mismatches 1
                                                                                                                                                                                                  RESULT 82
US-09-939-754-7
; Sequence 7, Application US/09939754
; Patent No. US20020051965A1
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Patent No. US20020127538A1
57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                      181 VMKIADF 187
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181 VMKIADF 187
                                                                         1 VMXVAEF 7
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US-09-939-832-7
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Publication No. US20030233675A1

Publication No. US20030233675A1

SERNEAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Gldman, Barry S.

PITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B.

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NO: 47374

SEQ ID NO 11118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10763418;
Publication No. US20040185547A1

GENERAL INFORMATION:
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TOWRENT FILING DATE: 2004-01-26
PRIOR PEPLING DATE: 2000-09-18
PRIOR FILING DATE: 1996-10-09
PRIOR FILING DATE: 1996-10-09
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 9
LENTH: 309
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                                                                    79.3%; Score 23; DB 16; Length 301; 57.1%; Pred. No. 1.4e+03; Live 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Methanosarcina mazei US-10-369-493-11118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                       Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
; ORGANISM: homo sapiens
US-10-470-957-21
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US-10-763-418-9
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176 VMKIADF 182
                                                                                                                                                                        1 VMXVAEF 7
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US-10-369-493-11118
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i Sequence 6, Application US/10763418

i Publication No. US20040185547A1

j Publication No. US20040185547A1

j GENERAL INFORMATION:

j APPLICANT: MOHAMMADI, MOOSA

j APPLICANT: HUBBARD, SIEVAN R.

TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

CURRENT APPLICATION NUMBER: US/10/763,418

CURRENT PILING DATE: 2004-01-26

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1099-11-09

PRIOR APPLICATION NUMBER: 08/701,191

PRIOR APPLICATION NUMBER: 08/701,191

PRIOR FILING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 16; Length 310;
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                 Length 310;
                                                                                                                                                                                                                                             Score 23; DB 16; Length 31
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
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Similarity 57.1%;
4; Conservative 5
                                                                                                                                                                                                                                                 Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                    SOFTWARE: Patentin Ver. 3.2; SEQ ID NO 27; LENGTH: 310; TYPE: PRT; ORGANISM: Homo sapiens US-10-664-421-27
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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181 VMKIADF 187
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181 VMKIADF 187
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Best Local Similarity
Matches 4; Conserv
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US-10-763-418-1
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Sequence 7, Application US/09939833

Sequence 7, Application US/09939833

GENERAL INFORMATION:
APPLICANT: WICKELE A.
APPLICANT: WICKESSHAM, OGHN A.
APPLICANT: PRACKSIAM, OGHN A.
APPLICANT: PRACKO, CHEIS.
APPLICANT: PRACKO, CHEIS.
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: APPELT, KRZYZZTOF
TITLE OF INVEWTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVEWTION: MODIFICATIONS OF USE
TITLE OF INVEWTION: METHODS OF USE
TITLE OF INVEWTION: METHODS OF USE
TITLE OF INVENTION: WETHODS OF USE
TITLE OF INVENTION NUMBER: US/09/939,833
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 1199-09-07
SEQ ID NO 7
LENGTH: 310
SEQ ID NO 7
LENGTH: 310
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                                                                                                                                                                                 79.3%; Score 23; DB 9; Length 310; 57.1%; Pred. No. 1.5e+03; tive 2; Mismatches 1; Indels
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US-10-664-421-27

$ Sequence 27, Application US/10664421

$ Publication No. US20040142864A1

$ Publication No. US20040142864A1

$ GENERAL INFORMATION:

$ APPLICANT: BREMER, RYAN

$ APPLICANT: KUMAR, ABHINAV

$ APPLICANT: MILBURN, MICHAEL V.

$ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

$ FILE REFERENCE: 039363/0703

$ CURRENT FILING DATE: 2003-09-16

$ PRIOR APPLICATION NUMBER: 60/412,341

$ PRIOR FILING DATE: 2002-09-20

$ PRIOR FILING DATE: 2002-09-16

$ PRIOR FILING DATE: 2002-09-16
                                                                                                                                                                                    Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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ses 4; Conservative
                    ; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-832-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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181 VMKIADF 187
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181 VMKIADF 187
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SEQ ID NO 7
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Gaps

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APPLICANT: Alsobrook II, John F
APPLICANT: Alsobrook II, John F
APPLICANT: Gerlach, Valerie I
APPLICANT: Gerlach, Valerie I
APPLICANT: Gerlach, Valerie I
APPLICANT: Macbougall, John R
APPLICANT: Mishra, Vishnu
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
ITILE OF INVENTION: NOVEL PROTEINS US/09/912,976
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: 60/221,336
PRIOR APPLICATION NUMBER: 60/238,333
PRIOR FILING DATE: 2000-10-05
PRIOR PELING DATE: 2001-01-05
PRIOR PELING DATE: 2001-01-05
PRIOR PELING DATE: 2001-01-05
PRIOR PELING DATE: 2001-02-23
PRIOR PELING DATE: 2001-03-23
PRIOR PELING DATE: 2001-03-23
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE
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US-10-774-355A
Sequence 2526, Application US/10774355A
Publication No. US20050043513A1
GENERAL INFORMATION:
APPLICANT: Firestein, Stuart
APPLICANT: Elang, Xinmin
TITLE OF INVENTION MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
FILE REFERENCE: A34570-PCT-USA-A 070050.2520
                                                                                                                                                                                            Score 23; DB 16; Length 310;
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
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Pred. No. 1.5e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09912976
Publication No. US20030212255A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mezes, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess, Catherine
Casman, Stacie
Grosse, William M
Alsobrook II, John P
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-10-763-418-8
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ORGANISM: Mus musculus
US-09-912-976-70
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181 VMKIADF 187
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US-09-912-976-70
   SEQ ID NO 8
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APPLICANT: MOHAMADI, MOOSA
APPLICANT: MOHAMADI, MOOSA
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE
FILE REPERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/10/763,418
CURRENT APPLICATION NUMBER: US/99/664,526
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR PILING DATE: 1996-11-09
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 7
LENGTH: 310
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Publication No. US20040185547A1

GENERAL INFORMATION:
APPLICANT: MOIAWAADI, MOOSA

APPLICANT: MOIAWAADI, MOOSA

APPLICANT: MOIAWAADI, MOOSA

APPLICANT: MOIAWAADI, MOOSA

APPLICANT: HUBBARD, STEVAN R.

TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: US/10/763,418

PRIOR APPLICATION NUMBER: US/10/64,526

PRIOR PILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTIN OF: 2.1
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79.3%; Score 23; DB 16; Length 310;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/10763418; Publication No. US20040185547A1; GENERAL INFORMATION:
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-763-418-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-763-418-7
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181 VMKIADF 187
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181 VMKIADF 187
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US-10-763-418-8
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                               SEQ ID NO 6
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                                                                  LENGTH:
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**Gaps** 

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Query Match
Best Local Similarity 42. 91
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Best Local Similarity 42.9
Matches 3; Conservative
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GORGANISM: Homo sapiens
US-10-017-161-1934
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba. Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TILLE OF INVENTION: TER, a No. US20030022278Alel Family of Taste Receptors
CURRENT APPLICATION NUMBER: US/09/510,332
CURRENT APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 44
LENGTH: 314
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Publication No. US20030022278A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278A1e1 Family of Taste Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 17; Length 312; 57.1%; Pred. No. 1.5e+03; ive 2; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/774,355A
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: PCT/USO2/25556
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
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US-09-510-332-44
Sequence 44, Application US/09510332;
Publication No. US20030022278A1;
GENERAL INFORMATION:
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Matches 4; Conservative
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Matches 3; Conservative
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11 ILAIAEF 17
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US-09-510-332-71
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| FILE REPERRORS, 03107E-08801008
| CURRENT PRICIATION NUMBER: 105/09/510,332
| CURRENT PRICIATION NUMBER: 105/09/510,334
| PRIOR APPLICATION NUMBER: 105/09/510
| CURRENT PRICIATION NUMBER: 105/09/510
| SAGMEND FILE STATES AND STAT
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Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative
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ORGANISM: Homo sapiens
US-10-770-127-71
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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   US-10-770-127-44
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Sequence 44, Application US/10770127

Publication No. US20040214239A1

GENERAL INFORMATION:

APPLICANT: SERVANT, GUY

APPLICANT: SERVANT, GUY

APPLICANT: BRUST, PAUL

APPLICANT: WINSTION: FUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEINS

TITLE OF INVENTION: FUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEINS

TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TIR

TITLE OF INVENTION: AND T2R MODULATORS

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Publication No. US20040067499A1
GENERAL INFORMATION:
APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR APPLICATION NUMBER: JP 2001/34434
SEQ ID NOS: 694
SOFTWARE: Patentin Ver. 2.1
LENGTH: 314
                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1478
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
NUMBER OF SEQ ID NOS: 2070
                                                                                                                                                                  ORGANISM: Homo sapiens
US-10-292-798-1478
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CORGANISM: Homo sapiens
US-10-343-650A-672
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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US-10-343-650A-672
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                                                                                                     LENGTH: 314
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Sequence 71, Application US/10770127

Sequence 71, Application US/10770127

Publication No. US20040214239A1

GENERAL INFORMATION:
APPLICANT: SERVANT, GUY
APPLICANT: SERVANT, GUY
APPLICANT: OZECK, MARK
APPLICANT: OZECK, MARK
APPLICANT: OZECK, MARK
APPLICANT: AV, HONG
ITILE OF INVENTION: AND T2R MODULATORS
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 60/444,172
PRIOR PELING DATE: 2003-02-03
PRIOR FILING DATE: 2003-02-03
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-05
SOFTWARE: Patentin version 3.2
SEQ ID NO 71
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US-10-962-365-44

Sequence 44, Application US/10962365

Publication No. US20050048586A1

GENERAL INFORMATION:
APPLICANT: Aler, Jon Elliot
APPLICANT: Aler, Jon Elliot
APPLICANT: Holer, Ken
APPLICANT: WHORER: US/10/962,365
CURRENT FILING DATE: 2004-10-07
FRIOR FILING DATE: 2000-22-2
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 44

LENGTH: 314
Query Match 79.3%; Score 23; DB 16; Length 314; Best Local Similarity 42.9%; Pred. No. 1.5e+03; Matches 3; Conservative 3; Mismatches 1; Indels
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Pred. No. 1.5e+03;
3; Mismatches 1;
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US-10-962-365-71
Sequence 71, Application US/10962365
Publication No. US20050048586A1
GENERAL INFORMATION:
APPLICANT: SALEY, Jon Elliot
APPLICANT: Adley, Jon Elliot
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents Of the University of STILE REPERENCE: 02307E-098010US
CURRENT PILION UNDER: US/10/962,365
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US/09/510,332
PRIOR APPLICATION NUMBER: US/09/510,332
PRIOR PILIOR DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 71
LENGTH: 314
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79.3%; Score 23; DB 17; Length 314;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels
; OTHER INFORMATION: human T2R24 (hGR24)
US-10-962-365-44
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US-10-962-365-71
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Sequence:

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                                                                                                 June 13, 2005, 13:36:32; Search time 24 Seconds (without alignments) 28.063 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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21 72.4 244 2 T13456 21 72.4 251 2 T29733 21 72.4 252 2 B66564 21 72.4 252 2 B66564 21 72.4 253 2 B66564 21 72.4 253 2 B66564 21 72.4 253 2 B66564 21 72.4 268 2 B72333 21 72.4 268 2 B72333 21 72.4 268 2 B72333 21 72.4 269 2 G72550 21 72.4 269 2 G72550 21 72.4 269 2 G72550 21 72.4 299 2 AC2030 21 72.4 299 2 T45662 21 72.4 299 2 AC2030 21 72.4 299 2 T45662 21 72.4 299 2 AC2030 21 72.4 299 2 AC2030 21 72.4 299 2 T45662 21 72.4 300 2 D30115 21 72.4 300 2 T10312 21 72.4 300 2 AD8159 21 72.4 300 2 AD8159 21 72.4 313 2 B84320 21 72.4 313 2 B84320 21 72.4 331 2 AC3665 21 72.4 331 2 AC3665 21 72.4 336 2 AC2666 21 72.4 336 2 AC2666 21 72.4 336 2 AC3666 21 72.4 356 2 AC3666 21 72.4 356 2 AC366 21 72.4 356 2 AC366 21 72.4 366 1 G499664 21 72.4 366 2 AF3398	R;Guirakhoo, F.; Heinz, P.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M. J. Gen. Virol. 72, 333-338, 1991  A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by mont A;Reference number: A61409; MUID:91132129; PMID:1847173  A;Recession: A61409  A;Status: not compared with conceptual translation A;Residues: 319-337 GUI> A;Residues: 877-994 GUI> C;Superfamily: yellow fever virus genome polyprotein C;Superfamily: yellow fever virus genome polyprotein C;Reywords: glycoprotein; nonstructural protein; nucleotide binding; P-loop; polyprotein, F;1-332/Product: nonstructural protein NS2# #status predicted <ns3> F;353-582/Product: nonstructural protein NS2# #status predicted <ns3> F;314-1334/Product: nonstructural protein NS2# #status predicted <ns3> F;312-919/Region: nucleotide-binding motif A; P-loop;</ns3></ns3></ns3>		
21	hypothetical hypothetical conserved by CT470 hypothe CT470 hypothe CT470 hypothe CT470 hypothe CT470 hypothe CT470 hypothe CT470 hypothetical probable auf hypothetical probable cari probable cari hypothetical hypothetical	nypotherical cytochrome-c 2'-hydroxyisc hypotherical hypotherical methyl violog dihydrodipicc dihydrodipicc dihydrodipicc hypotherical protein F7H2. phypotherical hypotherical hypotherical hypotherical hypotherical	SIMENTS
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deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Dacesion: E4205 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.I. Science 270, 397-403, 1995 Gaps || :||| 629 VMSIAEF 635 1 VMXVAEF 7 RESULT 3 E64205 ઠે 셤 A42545 genome polyprotein - Langat virus (strain TP21) (fragment) N:Contains: nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NSS

09730329-60ed.rpr

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Gaps

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2; Length 324;

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: UNIPROT:Q9ZPQ5; GB:AE002093; NID:G4406768; PIDN:AAD20079.1; GSPDB:GN(
C;Genetics:
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R;Kunst, F.; Ogaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A;Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Hujbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A;Authors: P.; Wipat, A.; Tanaka, T.; Terpeira, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yate, Erence number: A;Reference number: A;Reference number: A;Perference num
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R; Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1997
A; Recension: T38126
A; Recension: T38126
A; Recension: T38126
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A; Restauts: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-632 < RAD>
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-201 <KUN>
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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Pred. No. 42;
2; Mismatches 1; Indels
        A; Reference number: A84420; MUID: 20083487; PMID: 10617197
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36;
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Pred. No.
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A.Map position: 2
C.Superfamily: alcohol sulfotransferase
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Similarity 57.1%;
4; Conservative ;
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ilarity 71.4%;
Conservative
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IMDIAEF 29
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A,Title: The minimal gene complement of Mycoplasma genitalium.

A,Reference number: A64200; MUID:96026346; PMID:7569993

A,Accession: E64205

A,Accession: E64205

A,Residues: preliminary; nucleic acid sequence not shown; translation not shown
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A,Residues: 1-23 < TIGR>
A,Residues: 1-23 < TIGR>
A,Esperimental source: strain G-37
A,Experimental source: strain G-37
A,Genetics:
C,Genetics:
C,Genetics:
C,Superfamily: deoxyribose-phosphate aldolase
C,Keywords: aldehyde-lyase; carbon-carbon lyase
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probable steroid sulforransferase [imported] - Arabidopsis thaliana
probable steroid sulforransferase [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84452
C;Accession: B84452
C;Accession: B84452
C;Accession: B84452
C;Accession: B84452
C;Accession: B84452
M; Koo, H; Moffat, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-766, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
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A;Molecule type: DNA
A;Residues: 1-24 <LOE>
A;Residues: 1-24 <LOE>
A;Cross-references: UNIPROT: P09924; EMBL:X13544; NID:g44480; PIDN:CAA31897.1; PID:g44481
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 223;
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71.4%; Pred. No. 25;
cive 1; Mismatches
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C;Superfamily: deoxyribose-phosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase
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Best Local Similarity
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VMNIAEF 99
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217 VLDVAEF 223
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A;Note: L7610.5
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A,Cross-references: UNIPROT:P87111; EMBL:295334; PIDN:CAB08598.1; GSPDB:GN00066; SPDB:SF A;Experimental source: strain 972h-; cosmid c20G8
A;Genetics:
A;Genetics: SPDB:SPAC20G8.04c
A;Amap position: 1
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A; Molecule type: DNA
A; Molecule type: DNA
A; Rodesule type: DNA
A; Rossules: 1-195 «KUR»
A; Crossules: 1-195 «KUR»
A; Crossules: 1 UNIPROT: Q97F65; GB: AE001437; PIDN: AAK80830.1; PID: g15025935; GSPDB: GA: Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A41715; MUD:92105119; PMD:1840597
A;Accession: B41715
A;Crosse.references: UNIPROT:P29198; GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
C;Superfamily: ribosomal protein L13
                                                                                                                                                                                                                                                                                                                                                                                                                  ribosonal protein L13 [aimilarity] - Haloarcula marismortui
C;Species: Haloarcula marismortui
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: B41715
R;Kroemer, W.J.; Arndt, E.
A;Eloc. Chem. 266, 24573-24579, 1991
A;Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with bacterium) marismortui.
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Pred. No. 56;
0; Mismatches 1; Indels
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                                                                                                                                                 86.2%; Score 25; DB 2; Length 632; 71.4%; Pred. No. 1.3e+02;
                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                   1; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
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C,Superfamily: thymidine kinase
C,Keywords: phosphotransferase
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Matches 5; Conservative
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193 VMSLAEF 199
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131 LMAIAEF 137
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Best Local Similarity
Matches 4; Conserv
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MSVAEF 6
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Cipacesion: B70728
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rature 193, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome the Reference number: A70500; MulD:98295987; PMID:9634230
A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Residues: 1-236 <COL>
A;Residues: 1-236 <COL>
A;Cross-references: UNIPROT:050740; GB:277250; GB:AL123456; NID:g3261617; PIDN:CAB01046.JA;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18115
A;Reference number: Z18876
A;Reference number: Z18876
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-248 <OLI>
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A;Molecule type: DNA
A;Residues: 1-249 <TET>
A;Cross-references: UNIPROT:Q9PKD5; GB:AE002321; GB:AE002160; NID:g7190560; PIDN:AAF3937
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Ress. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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hypothetical protein Rv2558 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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Pred. No. 95;
1; Mismatches 1; Indels
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C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: F97010 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: F97010 #srooling, J.; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. #. Batteriol. 183, 4823-4838, 2001 #;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Closing A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Closing Bacteri
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A,Experimental source: Clostridium acetobutylicum ATCC824
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., A;Authors: Hunter, J.L.; Tiu, S.Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
                                                                                                                                                                                                                                                                                   tusion, chorismate mutase and shikimate 5-dehydrogenase [imported] - Clostridium acetobut
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C,Species: Aeropyrum pernix
C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86416
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Pred. No. 1.9e+02;
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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        1 VMXVAEF
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A;Status: preliminary
A;Molecule type: DNA
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437 VLQVAEF
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D97971
6-phosphofructokinase (EC 2.7.1.11) [imported] - Streptococcus pneumoniae (strain R6)
C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C.Accession: D97971
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; B. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; N. Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Releaus: prealiminary
A; Molecule type: DNA
A; Residues: 1-335 < KUR>
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C; Decise: Streptococcus pneumoniae
C; Decise: Streptococcus pneumoniae
C; Decise: Streptococcus pneumoniae
C; Decise: Streptococcus pneumoniae
C; Decisesion: F95103
C; Accession: F95103
Correspination, H.; Nelson, K.E.; Paulsen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2010
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Accession: F95103
A; Accession: F95103
A; Accession: F95103
A; Molecule type: DNA
A; Residues: 1-335 < KUR>
A; Residues: 1-335 < KUR>
A; Correspondent Bource: strain TIGRA
A; Experimental source: strain TIGRA
A;Experimental source: strain Nigg (MoPn)
(Senetics:
A;Gene: TCOS30
C;Superfamily: conserved hypothetical protein yloO; conserved hypothetical protein yloO
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A,Gene: SP0896
C,Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinas
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C;Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinas
C;Keywords: phosphotransferase
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                                                                                                                                                                                                            Length 249;
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                        Score 24; DB 2;
Pred. No. 96;
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Similarity 71.4%;
5; Conservative (
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
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A;Residues: 1-754 <JOH>
A;Cross-references: UNIPROT:P91063; EMBL:U80847; PIDN:AAB37983.1; GSPDB:GN00028; CESP:C17
A;Experimental source: strain Bristol N2; clone C17H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 8/3; 92/1; 142/1; 404/1; 437/1; 645/3
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
                                                                                                                                                                                                                                                                                                                          hypothetical protein C17H11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25551
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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A;Map position: X
A;Introns: 155/1; 246/3; 288/3; 368/3; 631/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C17H11.2
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         Length 584;
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                                                                 1; Indels
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      Score 24; DB 2; I
Pred. No. 2.2e+02;
2; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-919 <FUL>
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      Query Match 82.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                A;Tills: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 cKAM>
A;Cross-references: UNIPROT:Q9YE64; DDBJ:AP000060; NID:g5104188; PIDN:BAA79682.1; PID:g5
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E971052
hypothetical protein PH1116 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71052
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekirr
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71052
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
A;Gene: PH1116
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
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C;Species: Pyrococcus abyssi
C;Accession: F75090
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Accession: F75090
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A;Experimental source: strain Orsay
C;Genetics:
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A;Gene: APE0706
C;Superfamily: Archaeoglobus fulgidus probable DNA topoisomerase VI chain B
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Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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440 VMAIAEY 446
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A;Molecule type: DNA
A;Residues: 1-584 <KAW>
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28 MSVAEF 33
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03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A;Genome: plasmid pMT1
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C,Species: Bacillus halodurans
C,Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C,Accession: A83968
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83968
A;Accession: A83968
A;Accession: A83968
A;Accession: A83968
A;Accession: A83968
A;Gerecine: Treeliminary
A;Molecule type: DNA
A;Residues: 1-921 «STO»
A;Cross-references: UNIPROT:Q9K9V0; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB062
C;Genetics:
A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
NiAlternate names: isoleucyl-tRNA synthetase
C;Species: Bacillus subtilis
C;Species: bacillus subtilis
C;Species: bacillus subtilis
C;Daccession: H6543
E;Caccession: H6543
E;Encins: H6544
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A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
C;Superfamily: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
C;Keywords: aminoacyl-tRNA synthetase;
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83.3%; Pred. No. 3.5e+02;
ive 0; Mismatches 1; Indels
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Best Local Similarity
Matches 5; Conserv
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C;Accession: T42400
R;George, S.B.; Simokat, K.; Hardin, J.; Chisholm, A.D.
R;George, S.B.; Simokat, K.; Hardin, J.; Chisholm, A.D.
Cell 92, 633-643, 1998
A;Title: The VAB-1 Eph receptor tyrosine kinase functions in neural and epithelial morphota; Raference number: Z22158; MUID:98165343; PMID:9506518
A;Recession: T42400
A;Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CjAccession: AB3053
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellis class, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Beter, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB3577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Rosatiues: 1-96 «KUR»
A;Crosa-references: UNIPROT:08U8Q1; GB:AE008689; PIDN:AAL44840.1; PID:g17742484; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
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C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15018
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid A;Recession: T15018
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Reference number: John Spound Complete DNA Spound C
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Pred. No. 64;
0; Mismatches 1; Indels
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Genetics:

RESULT 24 T42bt receptor tyrosine kinase - Caenorhabditis elegans C;Species: Caenorhabditis elegans

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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69515
C;Accession: H69515
C;Accession: H69515
C;Accession: H69516
C;Accession: H69616

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C;Superfamily: riboflavin synthase beta chain
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote:
F;1-157/Domain: protein kinase homology (fragment) <KIN>
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C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86842
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A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Returns preliminary
A; Molecule type: DNA
A; Residues: 1-162 <STO>
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A;Experimental source: strain IL1403
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C;Accession: G00016
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C;Superfamily: shikimate kinase; shikimate kinase homology
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83.3%; Pred. No. 1e+02;
tive 0; Mismatches 1
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submitted to the EMBL Data Library, December 1995
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C;Species: Callithrix jacchus (common marmoset)
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Matches 5; Conservative
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A;Accession: G00016
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-143 < KLE>
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A; Residues: 1-157 <EIN>
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C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C; Accession: HB5912

R; Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Mature 409, 529-533, 2001

A; Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q8X7L7; GB:BA000007; PIDN:BAB36292.1; PID:g13362338; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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Pred. No. 80;
1; Mismatches 1; Indels
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                       A;Gene: Atu4039
A;Map position: linear chromosome
                                                                                                                                                 Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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52 ILNVAEF 58
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A;Residues: 1-112 <HAY>
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A; Residues: 1-112 <STO>
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A, Status: preliminary
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A;Gene: EC82869
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A,Gene: Z3230
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fibroblast growth factor receptor - Japanese medaka (fragment)
N;Contains: protein:-tyrosine kinase (EC 2.7.1.112)
C;Species: Oryxias latipes (Japanese medaka)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
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N.Contains: protein-tyrosine kinase (EC 2.7.1.112)

C.Species: Organs latipse (Japanese medaka)

C.Species: Organs latipse (Japanese medaka)

C.Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C.Accession: $27019

R.B. Baucka, A.; Saigo, K.

F.B. Lett. 134, 156-178, 1992

A.;Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).

A.;Reference number: $27019, MUD: 93093167; PMID: 1459248

A.;Reference number: $27019

A.;Graus not compared with conceptual translation

A.;Reference: UNIPROT: Q91176; GB: D13550; NID: 9222932; PIDN: BAA02749.1; PID: 9222933

A.;Cross references: UNIPROT: Q91176; GB: D13550; NID: 9222932; PIDN: BAA02749.1; PID: 9222933

C.;Superfamily: basic fibroblast growth factor receptor; magn

C.;Superfamily: basic fibroblast growth factor receptor; magn

F.1-172/Domain: protein kinase homology (fragment) are strucked for the factor receptor of the factor receptor of the factor receptor of the factor fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: ll-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2739
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Karo, P.; Romero, P.; Rant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8UPS5; GB:AE008688; PIDN:AAL42328.1; PID:g17739732; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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                                    Length 162
                                        Score 23; DB 2;
Pred. No. 1.2e+02;
                                                                                                                  1; Mismatches
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                                        79.3%;
Ouery Match
Best Local Similarity 66.7
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Matches 4; Conservative
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Matches 5; Conservative
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145 VMKIADF 151
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37 MTIAEF 42
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A,Molecule type: DNA
A,Residues: 1-169 <KUR>
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Cipacesion: S27022

R.Emori, Y.; Yasuoka, A.; Saigo, K.
FEBS Lett. 1314, 176-178, 1992

R.FEMORI, Y.; Yasuoka, A.; Saigo, K.
FEBS Lett. 1314, 176-178, 1992

A.Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).
A.Facesion: S27022

A.Facesion: 
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A;Molecule type: mRNA
A;Residues: 1.172 <ebno.
A;Cross-references: UNIPROT:Q02528; GB:D13552; NID:g222936; PIDN:BAA02751.1; PID:g222937
A;Cross-references: URIPROT:Q02528; GB:D13552; NID:g222936; PIDN:BAA02751.1; PID:g222937
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protesi
C;Keywords: alternative splicing; ATP; autophosphorylation; growth factor receptor; magne P:1.172/Domain: protein kinase homology (fragment) × KIN>
F:1.172/Domain: protein kinase homology (fragment) × KIN>
F:23.40, 132/Active site: Lys, Glu, Asp #status predicted
F:137,150/Binding site: magnesium (Asn, Asp) #status predicted
F:163/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Oryzias latipes (Japanese medaka)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C;Accession: S27021

R;Emori, Y: Ysavoka, A.; Saigo, K.

R;Emori, Y: Ysavoka, A.; Saigo, K.

A;Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).

A;Reference number: S27091

A;Reference number: S27091
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fibroblast growth factor receptor - Japanese medaka (fragment)
N;Contains: protein:-tyrosine kinase (EC 2.7.1.112)
C;Species: Orytias latipes (Japanese medaka)
C;Species: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
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C;Accession: S27020

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A; Experimental source: serogroup O1; strain N16961; biotype El Tor
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83.3%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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IMMVSEF 53
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Best Local Similarity
Matches 5; Conserv
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A;Gene: AGR C 2436
                                                       C;Genetics:
A;Gene: VCA0999
A;Map position: 2
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R; Emori, Y.; Yasuoka, A.; Saigo, K.
FEBS Lett. 314, 176-178, 1992
A; Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).
A; FREFERENCE number: 227019; MUID: 93093167; PMID: 1459248
A; Reference number: S27020
A; Reference number: S27020
A; Residues: not compared with conceptual translation
A; Residues: 1-172 < EMO>
A; Residues: 1-172 < EMO>
A; Residues: 1-172 < EMO>
A; Residues: 1-170 < EMO
A; 
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A;Molecule type: DNA
A;Residues: 1-191 <HEI>
A;Cross-references: UNIPROT:Q9KKV1; GB:AE004426; GB:AE003853; NID:g9658431; PIDN:AAF9689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         photosynthetic reaction center cytochrome c chain precursor - Erythrobacter sp. (fragmen C, Species: Brythrobacter sp. (fragmen C, Species: Brythrobacter sp. C, Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 C, Accession: S16314 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 C, Accession: S16314 hornberger, U.; Drews, G. Mol. Microbiol. 5, 1459-1468, 1991 A, Title: Organization of the genes coding for the reaction-centre L and M subunits and E
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C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82392
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R;Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.I. R.R.; Mekalanos, J.J.; Vonter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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Pred. No. 1.2e+02;
2; Mismatches 1;
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Best Local Similarity 83.3
Matches 5; Conservative
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145 VMKIADF 151
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Best Local Similarity
Matches 4; Conserv
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hypothetical protein AGR_C_2436 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C.Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: H97519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q8UFS5; GB:AE007869; PIDN:AAK87113.1; PID:g1516377; GSPDB:G?
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable tonB transport protein Cj0181 [imported] - Campylobacter jejuni (strain NCTC 11 C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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   Length 191;
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Pred. No. 1.8e+02;
2; Mismatches 1; Indels
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Score 23; DB 2; Length 191
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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Pred. No. 1.5e+02;
0; Mismatches 1
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C;Accession: 669479
R;Klenk, H.P.; Clayron, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.F. Elschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Mature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Rosidues: 1.231 *KLES.
A;Cross-references: UNIPROT:028438; GB:AE000976; GB:AE000782; NID:g2689299; PIDN:AAB8941:
C;Superfamily: Escherichia coli methionyl aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cl4 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Species: 2.4pr-1993 #sequence_revision 23-Apr-1993 #text_change 17-Nov-2000
C;Accession: F36819
R;Strayer, D.S.; Jerng, H.H.; O'Connor, K.
Virology 185, 585-595, 1991
A;Title: Sequence and analysis of a portion of the genomes of Shope fibroma virus and mal A;Reference number: A41700; MUID:92074222; PMID:1660196
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I.
I, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Residues: 1-373 <KUR>
A;Cross-references: UNIPROT:Q8ZESB; GB:AL590842; PIDN:CAC90887.1; PID:g15980086; GSPDB:GA
C;Genetics:
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 2.6e+02;
0; Mismatches 2; Indels
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A,Cross-references: GB:M32743
C;Superfamily: vaccinia virus nucleoside-triphosphatase I
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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A; Status: translation not shown
A; Molecule type: DNA
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C;Superfamily: ribonuclease D
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33 ILEVAEF 39
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F36819
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828749
NAD12 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - blue mussel mitochondrion (fragm C;Species: mitochondrion Mytilus edulis (blue mussel)
C;Species: mitochondrion Mytilus edulis (blue mussel)
C;Date: 22-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 828749; 82876
R;Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
Genetics 131, 39'-412, 1992
A;Title: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A;Reference number: $28743; MUID:92354892; PMID:1386586
                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-254 <BRS A;Cross-references: UNIPROT:P07283; EMBL:X03213; NID:g4444; PIDN:CAA26957.1; PID:g4445 A;Cross-references: UNIPROT:P07283; EMBL:X03213; NID:g4444; PIDN:CAA26957.1; PID:g4445 B;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu submitted to: he EMBL Data Library, May 1995 A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces of A;Reference number: S56186
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A,Residues; 1-254 <MUR>
A,Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09196.1; PID:g836710; GSPDB:GN0000
C,Genetics:
A,Gene: SGD:SEC53; MIPS:YFL045c
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C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                           phosphomannomutase (EC 5.4.2.8) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YFL045c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S05874; S56210
S;Bernstein, M.; Hoffmann, W.; Ammerer, G.; Schekman, R.
J. Cell Biol. 101, 2374-2382, 1985
A;Title: Characterization of a gene product (sec53p) required for protein assembly in A;Reference number: S05874; MUID:86059690; PMID:3905826
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C;Species: Archaeoglobus fulgidus
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A;Residues: 1-104;105-275 <BRO>
A;Cross-references: UNIPROT:Q00860; EMBL:M83758; EMBL:M83759
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A;Map position: 6L
C;Superfamily: SEC53 protein
C;Keywords: intramolecular transferase; isomerase
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Best Local Similarity 66.,
--- 4; Conservative
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A; Molecule type: DNA
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Matches 4
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R;Poulin, M.L.; Patrie, K.M.; Botelho, M.J.; Tassava, R.A.; Chiu, I.
Development 119, 333-361, 1993
A;Fitle: Heterogeneity in the expression of fibroblast growth factor receptors during lin
A;Reference number: I51023; MUID:94116439; PMID:8287792
                                                                                                                                                                                                                                                                                        C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protest C; Reywords: AFP; growth factor receptor F; 44-329/Domain: protein kinase homology < KINs F; 44-329/Domain: protein kinase ATP-binding motif
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75017
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A;Molecule type: DNA
A;Residues: 1-393 «KAW»
A;Cross-references: UNIPROT:Q9V088; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49817;
C;Genetics:
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pantothenate metabolism flavoprotein homolog homolog lmo1825 [imported] - Listeria monocy
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C;Date: 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Dates 20:Accession: Al1302
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, J. Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                           A/Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-388 <POU>
A,Cross-references: UNIPROT:Q91146; GB:L19868; NID:g476726; PIDN:AAA49394.1; PID:g476727
A,Genetics:
A,Genetics:
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C;Date: 20-Aug_1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Pred. No. 2.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: metB; PAB0605
C;Superfamily: O-succinylhomoserine (thiol)-lyase
C;Keywords: carbon-oxygen lyase; carbon-sulfur lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 VMKIADF 210
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Best Local Similarity
Matches 4; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <GLA>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Ereidues: 1-387 <STO>
A;Cross-references: UNIPROT:Q9HYM7; GB:AE004759; GB:AE004091; NID:g9949500; PIDN:AAG0676
A;Experimental source: strain PAOl
A;Genetics:
                                                                                                                                                                                                                                                                               genome polyprotein - tick-borne encephalitis virus (strain K23) (fragment)
N.Contains: membrane protein M; nonstructural protein NS1
Species: tick-borne encephalitis virus
C;Species: tick-borne encephalitis virus
C;Accession: A48352; S18104
C;Accession: A48352; S18104
C;Accession: A48352; S18104
C;Accession: A48352; S18104
Aritle: Sequence of the NS 1 gene of the K 23 isolate of tick-borne encephalitis virus
A;Reference number: A48352; MUD: 9328450; PMID: 8470955
A;Reference number: A48352
A;Residues: 1-377 <JACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q88482; EMBL;X62886; NID:g62032; PIDN:CAA44678.1; PID:g62033 A;Note: sequence extracted from NCBI backbone (NCBIP:129078) C;Superfamily: yellow fever virus genome polyprotein C;Keywords: membrane protein; nonstructural protein; polyprotein
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fibroblast growth factor receptor 1 - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51023
                                                         Gaps
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79.3%; Score 23; DB 2; Length 373; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 387;
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VFTVAEF 184
                                                                                                                                                         120 MLVAEF 125
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249 MAIAEF 254
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                        Best Local Similarity
Matches 5; Conser
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Matches 5; Conser
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Matches 4; Conser
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     Query Match
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A48352
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Length 415;

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B97213 fAD/FMN-containing dehydrogenase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum
   h 79.3%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                        || :|:|
233 VMKIADF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 MHVAEF 341
       Query Match
Best Local Similarity
Matches 4; Conserv
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-421 <KUR>
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C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Accession: 165223; 165226
R;Yan, G.; McBride, G.; McKeehan, W.L.
Biochem: Biophys. Res. Commun. 194, 512-518, 1993
A;Title: Exon skipping causes alteration of the COOH-terminus and deletion of the phosph A;Reference number: 152281; MUID:93326167; PMID:8333865
A;Accession: 16523
A;Accession: 16523
A;Accession: 16523
A;Accession: 16523
A;Accession: 16528
A;Accession: 16528
A;Accession: 16528
A;Accession: 16528
A;Accession: 1415 are anslated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-415 are anslated from GB/EMBL/DDBJ
A;Accession: 16528
A;Acce
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Al1674
particethenate metabolism flavoprotein homolog homolog lin1939 [imported] - Listeria innoc
C;Bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Al1674
C;Accession: Al1674
R;Glaser, P:, Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
:; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D:; Jones, L.M.; Karst, U.
Science 294, 849-845, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A,Authors: Rreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: Al1674
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: UNPROT:Q92Al3; GB:AL592022; PIDN:CAC97169.1; PID:gl6414440; GSPDB:G
C;Genetics:
C;Genetics:
A,Gene: lin1939
C;Superfamily: pantothenate metabolism flavoprotein dfp
A;Cross-references: UNIPROT:08Y674; GB:NC_003210; PIDN:CAC99903.1; PID:g16411279; GSPDB:A;Experimental source: strain EGD-e C;Genetics C;Genetics A;Gene: lmo1825 C;Superfamily: pantothenate metabolism flavoprotein dfp
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                                                                                                                                                                                                                                Query Match 79.3%; Score 23; DB 2; Length 399; Best Local Similarity 57.1%; Pred. No. 2.8e+02; Matches 4; Conservative 2; Mismatches 1; Indels
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171 VLRIAEF 177
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171 VLRIAEF 177
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C;Accession: A90003
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucha, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: UNIRROT:099SF8; GB:BA000018; PID:gl3701894; PIDN:BAB43186.1; GSPDB:GP.A;Experimental source: strain N315
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C;Species: T28015
R;Harris, B.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z20456
A;Accession: T28015
A;Accession: T28015
A;Accession: T28015
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-445 <WIL>
A;Residues: 1-445 <WIL>
A;Cross-references: UNIPROT:Q23615; EMBL:Z73898; PIDN:CAA98068.1; GSPDB:GN00022; CESP:ZKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein murA [imported] - Staphylococcus aureus (strain N315)
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A;Introns: 20/2; 56/2; 69/2; 87/2; 105/2; 123/2; 254/3; 272/3; 350/3
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                                                                      1; Indels
Score 23; DB 2;
Pred. No. 2.9e+02;
2; Mismatches 1
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probable hydrolase STY1503 [imported] - Salmonella enterica subsp. enterica serovar Typh C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AI0673
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servox. A;Reference number: AB0502; MUID:21534947; PMID:11677608
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A,Introns: 49/1; 91/3; 139/2; 179/2; 221/2; 270/1; 311/3; 342/2; 399/1; 481/1; 510/2; 55
C,Superfamily: ATP-binding cassette homology
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A; Cross-references: UNIPROT:076414; EMBL:AF067949; PIDN:AAC19238.1; GSPDB:GN00023; CESP:
A; Experimental source: strain Bristol N2; clone T10H9
        A,Gene: BMEI1382
A,Map position: I
C.Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C,Keywords: oxidoreductase
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C; Genetics:
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Pred. No. 3.5e+02;
0; Mismatches 2;
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llarity 71.4%; Pred. No. 4.2e+02;
Conservative 1; Mismatches 1;
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Pred. No. 4.2e+02;
2; Mismatches 1;
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57.1%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Matches 5; Conserv
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Best Local Similarity
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Residues: 1-484 <WIL>
A;Cross-references: UNIPROT:Q19704; EMBL:Z68336; PIDN:CAA92740.1; GSPDB:GN00022; CESP:F2
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betaine aldehyde dehydrogenase (EC 1.2.1.8) [imported] - Brucella melitensis (strain 16M C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3424
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97213
R;Nolling, J.; Bratch, G.; Muchence, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Benett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97213
A;Accession: B97213
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97213
A;Residues: preliminary
A;Residues: 1-467 <KUR>
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A,Experimental source: strain 16M
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21235
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Pred. No. 3.3e+02;
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    Caenorhabditis elegans

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Pred. No. 3.4e+02;
2; Mismatches 1;
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A;Accession: T21235
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 71/1; 135/3; 223/3; 247/1; 309/3; 396/3
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submitted to the EMBL Data Library, January 1996
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C,Superfamily: glycolate oxidase chain glcD
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ilarity 57.1%;
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T21235
hypothetical protein F22B3.8
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238 IMLVSEF 244
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Best Local Similarity
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Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-500 <KUR>
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A;Gene: CESP:F22B3.8
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submitted to the EMBL Data Library, December 1992
A;Description: Five additional avian Eph-related tyrosine kinases are differentially exp.
A;Reference number: S33502
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A;Status: preliminary
A;Status: breliminary
A;Status: breliminary
A;Status: breliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:Z19060
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc
C;Reywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kir:
F;63-147/Domain: fibronectin type III repeat homology <3FR>
F;45-513/Domain: protein kinase homology <4RN>
F;253-261/Region: protein kinase ATP-binding motif
F;536-602/Domain: SAM homology <5AM>
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Rivierman, W.C.; Feldblyuw, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Lauch, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonč
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Cauloboter crescentus.
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1450; PT0191
R;Horlick, R.A.; Stack, S.L.; Cooke, G.M.
Gene 120, 291-295, 1992
A;Title: Cloning, expression and tissue distribution of the gene encoding rat fibroblast
A;Reference number: JC1450; MUID:93013049; PMID:1398143
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A;Molecule type: mRNA
A;Residues: 1-650 (40R.>
A;Cross-references: UNIPROT:Q63709; GB:M91599; NID:g204137; PIDN:AAA41157.1; PID:g204138
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Neuron 6, 691-704, 1991
A;Tille: An extended family of protein-tyrosine kinase genes differentially expressed in
A;Reference number: PT0183; MUID:91222560; PMID:2025425
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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Pred. No. 4.3e+02;
0; Mismatches 2; Indels
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Pred. No. 4.4e+02;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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                                                                                                  A; Accession: S33506
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C.; Ma
                                                                                                                                                                            hypothetical protein B208.250 [imported] - Neurospora crassa C;Species: O-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: T49577
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49577
A;Status: preliminary
A;Solutie type: DNA
A;References: DNA
A;Residues: 1-604 <CCH>
A;CCOSS-references: UNIPROT: Q9P604; EMBL: AL355930; GSPDB: GN00116; NCSP: B208.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-609 <WHI>
A;Cross-references: UNIPROT:Q9RRC4; GB:AE002086; GB:AE000513; NID:g6460395; PIDN:AAF1210
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arginyl-tRNA synthetase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75257
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S;Sinth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Recession: B75257
A;Status: preliminary
A;Mocession: B75250; MUID:20036896; PMID:10567266
A;Status: preliminary
A;Mocession: B75257
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C;Species: Gallus gallus (chicken)
C;pacies: 2-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
C;Accession: S3566
R;Sajjadi, F.G.; Pasquale, E.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 604;
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C;Superfamily: Neurospora crassa hypothetical protein B208.250
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Pred. No. 4.3e+02;
1; Mismatches 1; Indels
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A,Gene: DR2568
A,Map position: 1
C,Superfamily: Bacillus arginine-tRNA ligase
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ilarity 71.4%;
Conservative
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277 IMDVSEF 283
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340 IMRVSEF 346
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A;Map position: 6
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S33506
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Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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516 VLNIAEF 522
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549 VMKIADF 555
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397 VIAIAEF 403
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A;Molecule type: mRNA
A;Residues: 1-682 <HAT>
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A; Residues: 465-588 <LAI>
A; Residues: 465-588 <LAI>
C; Generinental source: sciatic nerve
C; Generinental source: sciatic nerve
C; Generinental source: sciatic nerve
C; Genericus:
A; Gene: RGFR4; tyro-9
C; Function:
A; Dene: RGFR4; tyro-9
C; Function:
A; Dene: RGFR4; tyro-9
C; Function:
A; Dete: expressed in normal lung; expressed in some carcinomas
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology, rMD-
C; Reywords: AFP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F; 110-181/Domain: immunoglobulin homology <MD-
F; 110-181/Domain: immunoglobulin homology <MD-
F; 110-181/Domain: intransmembrane #status predicted <TWM-
F; 110-181/Domain: intracellular #status predicted <INT-
F; 113-598/Domain: protein kinase homology <KIN-
F; 121-329/Region: protein kinase AFP-binding motif
F; 121-329/Region: protein kinase AFP-binding motif
F; 121-329/Region: protein kinase AFP-binding motif
F; 135-137, 186, Bainding site: Lys, Glu, Asp #status predicted
F; 351, 368, 460/Active site: Lys, Glu, Asp #status predicted
F; 455, 478/Binding site: magnesium (Asn, Asp) #status predicted
F; 491/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q92IW1; GB:AE006914; PIDN:AAL02847.1; PID:g15619368; GSPDB:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 65
E97738
DNA topoisomerase (ATP-hydrolysing) (EC 5.99.1.3) - Rickettsia conorii (strain Malish 7)
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H71676
R;Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 36, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71676
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Ricketteia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97738
Science 293, 2003-2008, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97738
A;Accession: B97738
A;Accession: Conorii and Rickettsia prowazekii.
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%; Score 23; DB 1; Length 650, 57.1%; Pred. No. 4.6e+02; tive 2; Mismatches 1; Indels
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
C;Keywords: isomerase
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Matches 4; Conservative
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les 4; Conservative
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473 VMKIADF 479
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397 VISIAEF 403
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A,Cross-references: UNIPROT:Q92DU7; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14690
A;Experimental source: strain Madrid B
C;Genetics, Gorden B
A;Gene: gyrB1; RP227
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: AB2017
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
Nakezaki, S. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote-C;Keywords: ATP; autophosphorylation; growth factor receptor; heparin binding; phosphopror: R;83-444/Domain: immunoglobulin homology <IMN-F;88-674/Domain: protein kinase homology <IMN-F;88-674/Domain: protein kinase homology <IMN-F;89-674/Domain: protein kinase ATP-binding motif
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R;Hattori, Y.; Odagiri, H.; Nakatani, H.; Miyagawa, K.; Naito, K.; Sakamoto, H.; Katoh,
Proc. Natl. Acad. Sci. U.S.A. 87, 5983-5987, 1990
A;Title: K-sam, an amplified gene in stomach cancer, is a member of the heparin-binding
A;Reference number: A35969; WUID:90332706; PMID:2377625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two-component sensor histidine kinase all1688 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec_2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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C.Species: Homo sapiens (man)
C.Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                  Score 23; DB 2; I
Pred. No. 4.7e+02;
2; Mismatches 1;
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Pred. No. 4.8e+02;
2; Mismatches 1;
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C;Accession: A54846
R;Takagi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.
J;Biol. Chem. 269, 23743, 1994
A;Title: Molecular cloning and expression of the acidic fibroblast growth factor receptor ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors A;Reference number: A54846; MUID: 94375484; PMID: 8089146
A;Accession: A54846
A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-707 <TAK>
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protest C;Keywords: ATP; growth factor receptor P;57-118/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-713 <MAR>
A;Cross-references: UNIPROT:090330; EMBL:X76885; NID:g440139; PIDN:CAA54213.1; PID:g44014
C;Genetics:
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C,Species: Coturnix coturnix (quail)
C,Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Indels
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fibroblast growth factor receptor 1 beta-isoform - rat
C;Species: Rattus norvegicus (Norway rat)
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Pred. No. 5.1e+02;
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Pred. No. 5e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                               fibroblast growth factor receptor a precursor - rat
C;Species: Rattus norvegicus (Norway rat)
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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P;373-381/Region: protein kinase ATP-binding motif
   Mismatches
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ilarity 57.1%;
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525 VMKIADF 531
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                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1994
A, Reference number: S51634
A, Accession: S51635
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1705 < SAV>
A, Cross-references: EMBL: Z35138; NID: G551271; PIDN: CAA84510.1; PID: G551272
A, Accession: S51636
A, Accession: S51636
A, Accession: S51636
A, Molecule type: mRNA
A, Residues: 37-172, T7, 174-314, TV, 315-340, T', 342-705 < SA3>
A, Cross-references: EMBL: Z35139; NID: G551273; PIDN: CAA84511.1; PID: G551274
A, R, Savagner, P.; Valles, A.M.; Jouanneau, J.; Yamada, K.M.; Thiery, J.P.
Mol. Biol. Cell 5, 851-862, 1994
A, Title: Alternative splicing in fibroblast growth factor receptor 2 is associated with A, Accession: 348046; MUID: 95102150; PMID: 7803853
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A;Cross-references: RMBL:235138
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Reywords: ATP; growth factor receptor
C;Reywords: ATP; growth factor receptor
C;Reywords: ATP; growth factor receptor
F;57-118/Domain: immunoglobulin homology <IMM>
F;357-148/Domain: protein kinase homology <IMN>
F;355-648/Domain: protein kinase ATP-binding motif
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C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Date: 14-Feb-1992 #sequence_revision 1.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
R;Mikl, T.P. Fleming, T.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
Science 251, 72-75, 1991
A;Title: Expression cDNA cloning of the KGF receptor by creation of a transforming autoc
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Reywords: ATP; autophosphorylation; growth factor receptor; phosphoprotein; transmembr F;57-118/Domain: immunoglobulin homology <IMM>F;365-650/Domain: protein kinase homology <IMN>F;365-650/Domain: protein kinase homology «INN»
                                                                                                                           fibroblast growth factor receptor 2b, keratinocyte growth factor receptor - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jul-1995 #sequence revision 21-Jul-1995 #text_change 16-Jul-1999
C;Accession: S51635; S51636; $48048; S48047
R;Sayagner, P.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 37-135,'R',137-314,'TV',315-340,'T',342-390,'K',392-705 <SA2>
A;Cross-references: EMBL:235139
A;Accession: S48047
A;Status: preliminary; nucleic acid sequence not shown
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keratinocyte growth factor receptor precursor - mouse
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Pred. No. 5e+02;
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Best Local Similarity 57.1
Best Local 4, Conservative
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-707 <MIK>
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C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes
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Biochim. Biophys. Acta 1220, 209-211, 1994
A; Title: Nucleotide sequences of two newt (Notophthalmus viridescens) fibroblast growth 1
A; Reference number: S41050; MUID:94146117; PMID:8312364
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C.Superfamily: basic fibroblact growth factor receptor 1; immunoglobulin homology; protes
F;101-162/Domain: immunoglobulin homology <IMM>
F;408-693/Domain: protein kinase homology <KIN>
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F;488-496/Region: protein kinase ATP-binding motif
F;62-107,179-231,278-340/Disulfide bonds: #stetus predicted
F;62-107,179-231,278-340/Disulfide bonds: #stetus predicted
F;83,123,228,241,265,297,318,329,350/Binding site: carbohydrate (Asn) (covalent) #status
F;518,535,627/Active site: Lys, Glu, Asp #status predicted
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NyContains: protein-tyrosine kinase (BC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: S16236
R;Seno, M.; Sasada, R.; Watanabe, T.; Ishimaru, K.; Igarashi, K.
Biochim. Biophys. Acta 1089, 244-246, 1991
A;Title: Two cDNAs encoding novel human FGF receptor.
A;Reference number: S16236; MUID:91274356; PMID:1647213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibroblast growth factor receptor-2 - eastern newt
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41051
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                                                                                                                                                                      Score 23; DB 2; Length 748
Pred. No. 5.3e+02;
2; Mismatches 1; Indels
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Pred. No. 5.3e+02;
2; Mismatches 1;
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                                                   F;101-162/Domain: immunoglobulin homology <IMM>F;406-691/Domain: protein kinase homology <KIN>
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Best Local Similarity 57.1%;
Matches 4; Conservative
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566 VMKIADF 572
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Best Local Similarity
Matches 4; Conserv
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Residues: 1-769 <SEN>
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A, Status: prelimina
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 149293
R.Jin, Y.; Pasumarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 36, 149-1459, 1994
A.Title: Cloning and expression of fibroblast growth factor receptor-1 isoforms in the m. A.Reference number: 149289; MUID:95205422; PMID:7897669
A.Accession: 149293
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Steatus: preliminary; translated from GB/EMBL:U23445; NID:9733537; PIDN:AAC52183.1; PID:97335
A.Cross-references: UNIPROT:Q60830; EMBL:U23445; NID:9733537; PIDN:AAC52183.1; PID:97335
C.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology and the factor receptor 1; immunogl
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A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-729 < KIM>
A, Cross-references: UNIPROT: Q63827; GB: S54008; NID: g264804; PIDN: AAB54274.1; PID: g264805
A, Note: sequence extracted from NCBI backbone (NCBIN: 124259, NCBIP: 124270)
C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C, Keywords: alternative splicing; ATP; growth factor receptor
F;80-141/Domain: immunoglobulin homology < KIN>
F;301-399/Region: protein kinase homology < KIN>
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A56795
R;Kim, E.G.; Kwon, H.M.; Burrow, C.R.; Ballermann, B.J.
Am. J. Physiol. 264, F66-F73, 1993
Am. J. Physiol. 264, F66-F73, 1993
Am. J. Physiol. 264, F66-F73, 1993
A.Jitle: Expression of rat fibroblast growth factor receptor 1 as three splicing variant A;Reference number: A56795; MUID: 93158788; PMID: 8381605
A;Contents: Sprague-Dawley, kidneys
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 541050
R;Poulin, M.L.; Chiu, I.M.
Biochim. Biophys. Acta 1220, 209-211, 1994
A;Title: Nucleotide sequences of two newt (Notophthalmus viridescens) fibroblast growth A;Reference number: 541050, MUID:94146117; PMID:8312364
A;Accession: 541050
A;Accession: preliminary
A;Molecule type: MRNA
A;Residues: 1-748 <POU>
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57.1%; Pred. No. 5.2e+02;
iive 2; Mismatches 1,
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Best Local Similarity 57.1
Matches 4; Conservative
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543 VMKIADF 549
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VMKIADF 553
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A,Cross-references: UNIPROT:074504; EMBL:AL023705; NID:g3169070; PIDN:CAA19280.1; PID:g33. A,Experimental source: strain 9732.; cosmid c736
R;Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Rubmitted to the EMBL Data Library, September 1998
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A;Residues: 95-791 «RIE»
A;Cresimental source: EMBL:AL031523; NID:93560217; PIDN:CAA20660.1; PID:93560218; GSPDB:GNC
A;Experimental source: strain 972h-; cosmid c594
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C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 04-Feb-2000 C;Accession: A39627; S16679 K;Glazer, L; Shilo, B.Z. Genes Dev. 5, 697-705, 1991 A;Title: The Drosophila FGP-R homolog is expressed in the embryonic tracheal system and A;Reference number: A39627; MUID:91184623; PMID:1849109 A;Accession: A39627
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C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan.1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S3879
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A Modeleule typs: mRNA
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D. submitted to the EMBL Data Library, May 1998
A;Reference number: 221991
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Pred. No. 5.6e+02;
0; Mismatches 2; Indels
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Pred. No. 5.6e+02;
2; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-231 <WO>>
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A,Accession: T41445
A,Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Introns: 101/1; 131/2
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S38579
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Cispecies: Helicobacter pylori
Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
Cipatesion: Eds92
Cipatesion: Eds92
Cipatesion: Eds92
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Khalak, H.G.; Glodek, A.; McKenne
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Natitle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A6450; MuID:97394467; PMID:9252185
A; Reference number: A6450; MuID:97394467; PMID:9252185
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-773 <TOW>
A; Residues: 1-773 <TOW>
A; Residues: 1-773 <TOW>
A; Cross-references: UNIPROT:P55992; GB:AE000564; GB:AE000511; NID:g2313602; PIDN:AAD0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
B;Variety: L:Ring, B:L:Ring, B:L:Peb-1999 #text_change 09-Jul-2004
C;Accession: B71931
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature J97, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Accession: B71931
A;Status: preliminary
A;Residues: 1-773 <ARN>
A;Residues: 1-773 <ARN>
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A,Experimental source: strain J99
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N;Alternate names: fibroblast growth factor receptor
C;Species: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%; Score 23; DB 2; Length 773; ilarity 71.4%; Pred. No. 5.5e+02; Conservative 0; Mismatches 2; Indels
                                                     Indels
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A;Gene: gyrB
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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DNA gyrase, sub B - Helicobacter pylori (strain 26695)
             Pred. No. 5.4e+02;
2; Mismatches 1;
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DNA gyrase chain B - Helicobacter pylori (strain J99)
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        Best Local Similarity 57.1
Matches 4; Conservative
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640 VMKIADF 646
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Matches 5; Conserv
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Matches 5; Conserv
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A;Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2
A;Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2
A;Gene: GDB:127273; OMIM:176943
A;Gene: A;Gene: GDB:127273; OMIM:176943
A;Gene: GDB:127273; OMIM:176943
A;Gene: GDB:127273; OMIM:176943
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor; F;122-860/Product: fibroblast growth factor receptor fig-2 #status predicted <AGT>
E;22-860/Product: Eibroblast growth factor receptor fig-2 #status predicted <AGT>
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C,Accession: A48991
R;Katoh, O.; Hattori, Y.; Sasaki, H.; Sakamoto, H.; Fujimoto, K.; Fujii, T.; Sugimura, T
Cancer Res. 53, 1136-1141, 1933
A;Title: Isolation of the complementary DNA encoding a mouse heparin-binding growth fact
A;Reference number: A48991; MUID:93177694; PMID:8382556
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R;Avivi, A.; Zimmer, Y.; Yayon, A.; Yarden, Y.; Givol, D.
Orocgene 6, 1089-1092, 1991
A;Title: Flg-2, a new member of the family of fibroblast growth factor receptors. A;Reference number: A60350; MUID:91296390; PMID:1648703
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                                                                                                                                                                                                                                                                                                                                                                       fibroblast growth factor receptor flg-2 precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) flg-2 (5)Species: Homo sapiens (man) (C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
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C;Comment: This may be a receptor for keratinocyte growth factor
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N,Contains: protein-tyrosine kinase (EC 2.7.1.112)
C,Species: Mus musculus (house mouse)
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F;262-335/Domain: immunoglobulin homology <IMM>
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A;Molecule type: nucleic acid
                                                                                                                    622 VMKIADF 628
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624 VMKIADF 630
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                     1 VMXVAEF
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A; Residues: 1-485, (VVRAEAFG', 486-799 <STA2>
A; Residues: 1-485, (VVRAEAFG', 486-799 <STA2>
A; Residues: 1-485, (VVRAEAFG', 486-799 <STA2>
A; Cross-references: EMBL:X5927; NID:950968; PIDN:CAA42551.1; PID:950969
B; Gilardi-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson Oncogene 7, 2499-2506, 1992
A; Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the A; Reference number: S30496; MUID:93096484; PMID:1281307
A; Reference number: S30496; MUID:93096484; PMID:1281307
A; Reference signed: S10497
A; Reference Signed: S10496; MUID:93096484; PMID:1281307
A; Reference Signed: S10496
A; Residues: 611-667
CILA A; References: EMBL:X57236; NID:953187; PIDN:CAA40512.1; PID:953188
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C; Keywords: AFP; duplication; glycoprotein; growth factor receptor; phosphotransferase; F:1-18/Domain: signal sequence #status predicted <MAT>
F:19-799/Product: fibroblast growth factor receptor 4 #status predicted <MAT>
F:19-705/Domain: signal sequence #status predicted <MAT>
F:19-703/Product: fibroblast growth factor receptor 4 #status predicted <MAT>
F:19-703/Froduct: fibroblast predicted <MAT>
F:10-703/Froduct: fibroblast growth factor receptor 5 #status predicted <MAT>
F:10-703/Froduct: fibroblast growth factor receptor 7 #status predicted <MAT>
F:10-703/Froduct: fibroblast growth factor receptor 7 #status predicted <MAT>
F:10-703/Froduct: fibroblast growth factor receptor 7 #status predicted <MAT>
F:10-703/Froduct: Fibroblast growth factor receptor 7 #status predicted <MAT>
F:10-703/Froduct: Fibroblast growth factor receptor 8 #status predicted <MAT>
F:10-703/Froduct: Fibroblast growth factor face factor 7 #status predicted <MAT>
F:10-703/Froduct: Fibroblast growth factor face factor 7 #status factor 7 #status factor 7 #status 
R;Shi, D.L.; Fromentoux, V.; Launay, C.; Umbhauer, M.; Boucaut, J.C.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38579
A;Reference number: S38579
A;Accession: S38579
A;Accession: S38579
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-77
A;Re
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N;Contains: protein-tyrosine kinase Mpk-11
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus muculus (house mouse)
C;Species: Mus muculus (house mouse)
C;Accession: 518209, 526751; 530497
C;Accession: 518209, 526751; 530497
Development 113, 641-651, 1991
A;Title: FGPR-4, a new member of the fibroblast growth factor receptor family, expressed A;Reference number: $18209; MUID:92146274; PMID:1723680
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
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F;470-478/Region: protein kinase ATP-binding motif
F;54-98,169-221,268-330/Disulfide bonds: #status predicted
F;500,517,609/Active site: Lys, Glu, Asp #status predicted
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F;367-387/Domain: transmembrane #status predicted <TMMs
F;388-799/Domain: intracellular #status predicted <INT>
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57.1%; Pred. No. 5.6e+02;
iive 2; Mismatches 1.
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R,Stark, K.L.
Bubmitted to the EMBL Data Library, May 1991
A,Reference number: S26751
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Matches 4; Conservative
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Best Local Similarity
4; Conserve
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616 VMKIADF 622
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fibroblast growth factor
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A; Residues: 1-799 <STAl>
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-296, Dr. 298-802 <RON
A;Experimental source: mammary epithelial cell line B5/589
A;Note: binds acidic and basic fibroblast growth factors with high affinity R;Note: binds acidic and basic fibroblast growth factors with high affinity R;Note: U; Sreaminger, A; Strebhardt, K.; Ruebsamen-Waigmann, H. Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991
A;Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member c A;Reference number: S19025; MUID:92073297; PMID:1720539
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Cyfunction:

Cyfunction:

A,Description:

A,Note: expressed in normal lung; expressed in some carcinomas

C,Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes)

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes)

C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;

F;12-400main: signal sequence #status predicted <SIG.

F;25-802/Product: fibroblast growth factor receptor 4 #status predicted <MAT>

F;25-369/Domain: extracellular #status predicted <SIG.

F;50-103/Domain: immunoglobulin homology <IM3>

F;50-103/Domain: immunoglobulin homology <IM3>

F;30-390/Domain: immunoglobulin homology <IM3>

F;310-802/Domain: intracellular #status predicted <INT>
F;310-802/Domain: protein kinase homology <IM3>
F;310-802/Domain: protein kinase homology <IM3>
F;310-802/Domain: protein kinase ATP-binding mobif F;57-101,172-224,271-333/Disulfide bonds: #status predicted

F;5112,258,290,311,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;617,630/Sinding site: lys, Glu, Asp #status predicted

F;617,630/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

F;643/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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                                    A,Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic A,Reference number: A46615; MUID:93194827; PMID:7680645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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A; Residues: 399-534, W',536-799,'SG',800-802 <HOL>
A; Experimental source: lung
B; Partanen, J; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A; Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A; Reference number: A38268; MUID:91062389; PMID:2247464
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Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels
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A;Residues: 614-670 <PA2>
A;Cross-references: GB:M37781
A;Experimental source: K-562 leukemia cell line
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A,Cross-references: GDB:127929; OMIM:134935
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R;Chellaiah, A.T.; McEwen, D.G.; Werner, S.; Xu, J.; Ornitz, D.M.
J. Biol. Chem. 269, 11620-11627, 1994
A;Title: Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in immunoglobu A;Reference number: A53627; MUID:94209351; PMID:7512569
A;Accession: B53627
A;Status: preliminary
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A; Residues: 1-802 < PAR.>
A; Cross-references: UNIPROT: P22455; EMBL: X57205; NID: 931371; PIDN: CAA40490.1; PID: 931372
A; Note: binds acidic but not basic fibroblast growth factor with high affinity
R; Ron, D.; Reich, R.; Chedid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Miki
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AjIntrons: 304/3; 353/1
AjIntrons: 304/3; 353/1
AjIntrons: 304/3; 353/1
Cj.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote Cj.Keywords: ATP; growth factor receptor
F;262-335/Domain: immunoglobulin homology <IMM>
F;262-335/Domain: protein kinase homology <INM>
F;464-750/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast growth factor receptor 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 155363; B53627
R;Ornitz, D.M.; Leder, P.
B;Ornitz, D.M.; Leder, P.
A;Title: Ligand specificity and heparin dependence of fibroblast growth factor receptore A;Reference number: 155363; MUID:9235591; PMID:1379594
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                                                                                                                                                          79.3%; Score 23; DB 2; Length 800 ilarity 57.1%; Pred. No. 5.7e+02; Conservative 2; Mismatches 1; Indels
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F;262-335/Domain: immunoglobulin homology <IMM>F;464-749/Domain: protein kinase homology <KIN>F;472-480/Region: protein kinase ATP-binding motif
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A,Residues: 242-364 <CHE>
A,Cross-references: GB:L26492
C,Genetics:
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624 VMKIADF 630
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les 4; Conserv
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A; Residues: 1-801 <RES>
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote: C;Superfamily: hattophosphorylation; duplication; glycoprotein; growth factor receptor; C;Reywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor; F;1-23/emain: signal sequence #status predicted <SIG> F;24-806/Product: protein-tyrosine kinase cak2 #status predicted <MAT> F;24-368/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig. 13.1.138/Region: acidic
Fi262-335/Domain: immunoglobulin homology <IVM>
Fi369-389/Domain: transmembrane #status predicted <TVM>
Fi390-886/Domain: intracellular #status predicted <IVM>
Fi390-886/Domain: protein kinase homology <KIN>
Fi464-749/Domain: protein kinase homology <KIN>
Fi461-107,170-222,269-333/Disulfide bonds: #status predicted
Fi61-107,170-222,269-333/Disulfide bonds: #status predicted
Fi61-107,170-222,269-333/Disulfide bonds: #status predicted
Fi61-205,519/Binding site: magnesium (Ban, Asp) #status predicted
Fi616,529/Binding site: magnesium (Ban, Asp) #status predicted
Fi616,529/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predictec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibroblast growth factor receptor Al precursor - African clawed frog
N.Contains fibroblast growth factor receptor Al, short splice form; protein-tyrosine kir
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Feb_1992 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A39752; B39752
R;Friesel, R.; Dawid, I.B.
Rol. Cell. Biol. 11, 2481-2488, 1991
A;Title: CDNA cloning and developmental expression of fibroblast growth factor receptors A;Reference number: A39752; MUID:91203867; PMID:1850097
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A;Molecule type: mRNA
A;Residues: 1-814 < FRI>
A;Crosesion: B39752
A;Crosesion: B39752
A;Crosesion: B39752
A;Accession: B39752
A;Molecule type: mRNA
A;Residues: 1-30,119-814 < FR2>
A;Crosesion: B39752
A;Molecule type: mRNA
A;Residues: 1-30,119-814 < FR2>
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protest C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;1-21/Domain: signal sequence #status predicted <SIG>
;22-814/Product: fibroblast growth factor receptor Al, long splice form #status experime;22-372/Domain: extracellular #status predicted <EXT>
;22-372/Domain: extracellular #status predicted <EXT>
;22-30.119-814/Product: fibroblast growth factor receptor Al, short splice form #status;47-102/Domain: immunoglobulin homology <IM1>
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Fig. 86.77/Domain: protein kinase homology «KIN»
Fig. 86.77/Domain: protein kinase ATP-binding motif
Fig. 86.716,116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent) #ste Fig. 105,27,619/Active site: Lys, Glu, Asp #status predicted
Fig. 85.77,619/Active site: magnesium (Asn, Asp) #status predicted
Fig. 85.77/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicter
                                                                                                                                                                                                              A;Cross-references: UNIPROT:P18460; GB:M35195; NID:g211442; PIDN:AAA48664.1; PID:g211443
C;Genetics:
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1266-339/Domain: immunoglobulin homology <IM3>
1373-399/Domain: irransmembrane #status predicted <ITM>
1394-814/Domain: intracellular #status predicted <ITM>
                                     A;Reference number: A35963; MUID:90332672; PMID:2165604
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624 VMKIADF 630
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                                                                                                                                                                                             A; Residues: 1-806 <PAS>
                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
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Althocossion: A38578

Althocossion: A38578

Althocossion: WIRPOT: P22607; GB:WS8051; NID:g180568; PIDN:AMAS2450.1; PID:g182568

Althocossion: LW:PP Minners. S.; Schalling, M.; Althorr, M.R.; Gusella, J.P.; Housman, D.E.

Genomics 11, 1131-1142, 1991

Affille: A gene encoding a fibroblast growth factor receptor isolated from the Huntingtc

Althocossion: A5273

Alth
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C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A55963
R;Pasquale, B.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990
A;Title: A distinctive family of embryonic protein-tyrosine kinase receptors.
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57.1%; Pred. No. 5.7e+02;
ive 2; Mismatches 1; Indels
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Best Local Similarity 5/...
4; Conservative
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RESULT 89 A35963

09730329-60ed.rpr

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A/Status: mucleic acid sequence not shown, not compared with conceptual translation A/Status: mcNa A/Molecule type: mRNA A/Residues: 1-819 <LEE> A/Cross-references: UNIPROT: P21804 A/Aroces references: UNIPROT: P21804 A/Note: part of the sequence was confirmed by protein sequencing R/Pasquale, E.B.; Singer, S.J. Proc. Natl. Acad. Sci. U.S.A. 86, 5449-5453, 1989 A/Title: Identification of a developmentally regulated protein-tyrosine kinase by using & A/Accession: A33908, MUID:89315814; PMID:2473471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibroblast growth factor receptor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Daccies: Musr-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: S17295 R;Raz, V.; Kelman, Z.; Avivi, A.; Neufeld, G.; Givol, D.; Yarden, Y. Oncogene 6, T53-760, 1991 A;Fille: PCR-based identification of new receptors: molecular cloning of a receptor for i A;Reference number: S17295; MUID:91270892; PMID:1711190
                                                                                                                                                                                                                                                                                                                                                                                   CJACCESSION: A41345; A33908
R;Lee, P.L.; Johnson, D.E.; Cousens, L.S.; Fried, V.A.; Williams, L.T.
Science 245, 57-60, 1989
A;Title: Purification and complementary DNA cloning of a receptor for basic fibroblast g: A;Reference number: A41345; MUID:89298406; PMID:2544996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: this protein is expressed in embryonic tissues and, at low levels, in adult brair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                            fibroblast growth factor receptor 1 precursor - chicken
NiAlternate names: basic fibroblast growth factor receptor
NiContains: protein-tyrosine kinase (EC 2.7.1.112) cek1
Cispecies: Gallus gallus (chicken)
Cispecies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-89,'A',91-685,'M',687-819 <PAS>
A;Cross-references: GB:M24637
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634 VMKIADF 640
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637 VMKIADF 643
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Matches 4; Conserv
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   1 VMXVAEF
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A; Status: preliminary
A; Molecule type: mRNA
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S17295
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G4058

G4058

G4058

G5059

G5
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C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Accession: A49151
R;Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.
Development 116, 261-273, 1992
A;Title: Differential expression and regulation of two distinct fibroblast growth factor
A;Reference number: A49151; MUID:93130775; PMID:1483392
A;Rotession: A49151
A;Residues: Preliminary
A;Molecule type: nucleic acid
A;Residues: 1-816 cSHI>
A;Kesidues: 1-816 cSHI>
A;Kesidues: Growth factor receptor I; immunoglobulin homology; prote
C;Keywords: AFP; growth factor receptor
F;G9-230/Domain: immunoglobulin homology cINN>
F;472-757/Domain: protein kinase homology cKIN>
F;480-488/Region: protein kinase ATP-binding motif
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                            Length 814;
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                               Score 23; DB 1; 1
Pred. No. 5.8e+02;
                                                                                                  2; Mismatches
                        79.3%;
57.1%;
Query Match
Best Local Similarity 57.1.
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Best Local Similarity 57.1
Matches 4; Conservative
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632 VMKIADF 638
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Score 23; DB 1; Length 821; Pred. No. 5.8e+02; 2; Mismatches 1; Indels

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Fig. 233/Domain: immunoglobulin homology <IMM>
Fig. 233/Domain: immunoglobulin homology <IMM>
Fig. 298/Domain: immunoglobulin perdicted <TWM>
Fig. 398/Domain: intracellular #status predicted <INT>
Fig. 398/Domain: intracellular #status predicted <INT>
Fig. 398/Fig. 300 main: protein kinase homology <KIN>
Fig. 487-495/Region: protein kinase Arp-binding moif
Fig. 2107,179-231,278-442/Disulfide bonds: #status predicted
Fig. 228,241,265,297,318,331/Binding site: carbohydrate (Asn) (covalent) #status prec
Fig. 517,534,626/Active site: Lys, Glu, Asp #status predicted
Fig. 31,644/Binding site: magnesium (Asn, Asp) #status predicted
Fig. 57/Reinding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predictec
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NyAlternate names: bek transforming protein; fibroblast growth factor receptor 2; keratir
NyContains: protein-tyrosine kinase (EC 2.7.1.112) bek
C;Species: Mus musculus (house mouse)
C;Date: 30-un-1991 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: A44142; A31378
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R;Kornbluth, S.; Paulson, K.E.; Hanafusa, H.
RnJ. Cell. Biol. 8, 5541-5544, 1988
A;Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA A;Reference number: A31378; MUID:89219016; PMID:2468999
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Residues: 1-821 «MAN»
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;Residues: 477-821 <KOR>
;Cross-references: GB:M23362; NID:g533219; PIDN:AAA37285.1; PID:g533220
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Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels
extracellular #status predicted <EXT>
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639 VMKIADF 645
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                                                                                  F;132-138/Region: acidic
F;172-233/Domain: immuno
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                                                         A;Cross-references: UNIPROT:P21803; EMBL:X55441; NID:g50141; PIDN:CAA39083.1; PID:g50142 (Subgerfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote F;270-343/Domain: immunoglobulin homology <IMM> F;270-3743/Domain: protein kinase homology <IMN> F;478-763/Domain: protein kinase homology <IMN>
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A; Residues: 1-821 <DIO>
A; Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374
A; Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374
R; Houssaint, E.; Blanquet, P.R.; Champion-Arnaud, P.; Gesnel, M.C.; Torriglia, A.; Court
Proc. Natl. Acad. Sci. U.S.A. 87, 8180-8184, 1990
A; Title: Related fibroblast growth factor receptor genes exist in the human genome.
A; Reference number: A36210; MUID:91045961; PMID:2172978
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A,Molecule type: mRNA
A,COSS references: GB:MS5614, GB:M37715, NID:g339710, PIDN:AAA61188.1; PID:g339711
A,COSS reference mumber: A44775, MUD:91296403; PMID:1648704
A,Reference number: A44775, MUD:91296403; PMID:1648704
A,Residues: 263-361 < CH2>
A,Residues: 263-361 < 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 10q25.3-10q26
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
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A; Molecule type: mRNA
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A;Cross-references: GB:S41873
C;Comment: This receptor binds basic fibroblast growth factor and, with lower affinity,
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Pred. No. 5.8e+02;
2; Mismatches 1;
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A,Gene: GDB:FGFR2
A,Cross-references: GDB:127273; OMIM:176943
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57.1%;
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Matches 4, Conservative
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VMKIADF 644
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A;Residues: 1-820 <RAZ>
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Length 821;

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A;Molecule type: mRNA
A;Residues: 201-671, IYLTGS',677-822 <RUT>
A;Crost-references: EMBL:Y00665
R;Hattori, Y.; Odagiri, H.; Katch, O.; Sakamoto, H.; Morita, T.; Shimotohno, K.; Tobinai,
Cancer Res. 52, 3367-3371, 1992
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jRusnati, M. j Coltrini, D.; Caccia, P.; Dell'Era, P.; Zoppetti, G.; Oreste, P.; Valsasir

jRusnati, M. j Coltrini, D.; Caccia, P.; Dell'Era, P.; Zoppetti, G.; Oreste, P.; Valsasir

jRusnati, M. j Coltrini, D.; Caccia, P.; Dell'Era, P.; Zoppetti, G.; Oreste, P.; Valsasir

jRusnati, M.; Coltrini, D.; Caccia, P.; And 6-0-enlfate groups of heparin in the formation of

jRusnatic role of 2-0-, N-, and 6-0-enlfate groups of heparin in the formation of

jRusnatic role of 2-0-, N-, And 6-0-enlfate groups of heparin in the formation of
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A;Map position: 8p11.2-8p11.1
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gryrosine-specific protein kinase
A;Cross-references: EMBL:X57119; NID:g31388; PIDN:CAA40401.1; PID:g31389
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro;
A;Note: this form is designated isoform II
A;Accession: $17377
                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro; A;Note: this form is designated isoform III A;Accession: S17376
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A; Residues: 1-90, 'D', 91-147,150-822 <EIS>
A; Residues: 1-90, 'D', 91-147,150-822 <EIS>
A; Cross-references: EMBL: X57120
A; Note: this form is designated isoform IV
B; Itch, N.; Terachi, T.; Ohta, M.; Seo, M.K.
Biochem. Biophys. Res. Commun. 169, 680-685, 1990
A; Title: The complete amino acid sequence of the shorter form of human basic fibroblast A; Reference number: A35479; MUID: 90290512; PMID: 2162671
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A; Residues: 1-30,120-147,150-468,'L',470-822 < ITO>
A; Cross-references: GB:M37722; NID:9179413; PIDN:AAA75007.1; PID:9179415
A; Cross-references: GB:M37722; NID:9179413; PIDN:AAA75007.1; PID:9179415
A; Note: both the longer and shorter forms are expressed in the placenta
R; Johnson, D.E.; Lee, P.L.; Lu, J.; Williams, L.T.
Mol. Cell. Biol. 10, 4728-4736, 1990
A; Title: Diverse forms of a receptor for acidic and basic fibroblast growth factors.
A; Reference number: A36464; WUID:90355989; PMID:2167437
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;Ruta, M.; Howk, R.; Ricca, G.; Drohan, W.; Zabelshansky, M.; Laureys, G.; Barton, acogene 3, 9-15, 1988
ncogene 3, 9-15, 1988
;Title: A novel protein tyrosine kinase gene whose expression is modulated during e;Reference number: A28361
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Residues: 1-30,120-822 <JOH>
; Cross-references: GB:M34185; NID:g182531; PIDN:AAA35836.1; PID:g182532
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;Residues: 1-30,120-147,150-191,'E',193-822 <JO2>
;Cross-references: GB:M34186; NID:g182533; PIDN:AAA35837.1; PID:g182534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: not compared with conceptual translation Molecule type: DNA
                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-90,'D',91-822 <EI2
A;Cross-references: EMBL:X57121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein; Residues: 81-100 <RUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: PC2394
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A, ACCEGERION IS AGAIN M. M. MCKECHAN, K.; MCBCIAGA, G.; Adams, P.; MCKECHAN, W.L.

B, AGINE IS 1166.

A, ACCEGERION IS 1169.

      fibroblast growth factor receptor 1 precursor - human N;Alternate names: basic fibroblast growth factor receptor; heparin-binding growth factor X;Alternate names: basic fibroblast growth factor receptor; heparin-binding growth factor cypecies: Homo sapiens (man) Higgram bl; Higgram bl; Higgram al; Higgram C;Species: Homo sapiens (man) Higgram cypecies: Homo sapiens (man) Higgram al; Higgram C;Species: Homo sapiens (man) Higgram cypecies: Higgram cypecies: Higgram cypecies: Higgram cypecies: Higgram cypecies: Cy
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A; Residues: 1-30,120-147,150-822 <EI4>
A; Cross-references: EMBL:X57122; NID:931386; PIDN:CAA40404.1; PID:931387
A; Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro
A; Note: this form is designated isoform I
A; A; Accession: S17375
A; Molecule type: mRNA
A; Residues: 1-30,120-822 <EI3>
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A; Residues: 1-822 < TRL>
A; Residues: 1-822 < TRL>
A; Accession: S26738
A; Accession: S26738
A; Molecule type: mRNA
A; Residues: 1-47,152 < TR2>
A; Roselidues: 1-47,152 < TR2>
A; Residues: 1-47,152 < TR2>
A; Residues: 1-147,152 < TR2>
A; Residues: 1-147,152 < TR2>
A; Risiemann, A.; Ahn, J.A.; Graziani, G.; Tronick, S.R.; Ron, D.
Oncogene 6, 1195-1202, 1991
A; Title: Alternative splicing generates at least five different isoforms of the human b; Reference number: S1373; MulD:91319400; PMID:1650441
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D.E.

09730329-60ed.rpr

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1-30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-755,'R',757-764,'I
                                                              A,Cross-references: GB:M33760; NID:g193299; PIDN:AAA37622.1; PID:g309240
R,Harada, T.; Saitot, H.; Kouhara, H.; Kurebayashi, S.; Kasayama, S.; Terakawa, N.; Kishin Biochem. Biochem. Biochem. Elophys. Res. Commun. 205, 1057-1063, 1994
A,Title: Muxine fibroblast growth factor receptor 1 gene generates multiple messenger RNJ A,Teference number: PC2277; MUID:95100926; PMID:7802632
A,Reference number: PC2277
A,Molecule type: DNA
A,Residues: 1-15 <HAR>
A,Residues: 1-15 <HAR>
A,Cross-references: GB:S74765; NID:g833887; PIDN:AAB32845.1; PID:g833889
C,Comment: This protein mediates the biological actions of heparin-binding growth factors C,Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein C,Reywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;22-822/Product: fibroblast growth factor receptor 1 #status predicted <8IG>
F;22-376/Domain: extracellular #status predicted <8XT>
F;22-30,120-822/Product: fibroblast growth factor receptor 1 #status predicted <WAT>
F;22-30,120-822/Product: fibroblast growth factor receptor 1, short form #status predicte F;122-30,120-822/Domain: immunoglobulin homology <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              First 1337 Negation: occasion occasion occasion occasion occasion immunoglobulin homology <IMM>
Fi377-397/Domain: transmembrane #status predicted <IMM>
Fi398-822/Domain: intracellular #status predicted <INT>
Fi398-822/Domain: intracellular #status predicted <INT>
Fi484-492/Region: protein kinase Arp-binding motif
Fi484-492/Region: protein kinase Arp-binding motif
Fi55-101,178-230,277-341/Disulfide bonds: #status predicted
Fi55-102,272,240,246,256,317,330/Binding site: carbohydrate (Asn) (covalent) #status precipitation site: Lys, Glu, Asp #status predicted
Fi54,531,623/Active site: magnesium (Asn, Asp) #status predicted
Fi568,641/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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R;Takagi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.
R;Takagi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.
J. Biol. Chem. 269, 23743-23749, 1994
A;Title: Molecular cloning and expression of the acidic fibroblast growth factor receptor ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors. A;Reference number. A54846; MUID:94375484; PMID:8089146
A;Accession: B54846
A;Accession: B54846
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule fype: mRNA
A;Residues: 1-822 < TAK>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: B54846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 5.8e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: ATP; growth factor receptor
$1.72-233/Domain: immunoglobulin homology <IMM>
F;480-765/Domain: protein kinase homology <KIN>
F;488-496/Region: protein kinase ATP-binding motif
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640 VMKIADF 646
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Best Local Similarity
Matches 4; Conserv
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-822/Product: fibroblast growth factor receptor 1, form alpha al #status predicted < F;22-822/Product: fibroblast growth factor receptor 1, form alpha bl #status predicted <F;22-376/Domain: extracellular #status predicted <EXT>
F;22-147,150-822/Product: fibroblast growth factor receptor 1, form 3 #status predicted F;22-147,150-822/Product: fibroblast growth factor receptor 1, form beta al #status predicted F;22-30,120-427,430-822/Product: fibroblast growth factor receptor 1, form beta al #status predicted F;126-133/Region: acidic
F;161-822/Product: fibroblast growth factor receptor 1, form gamma al #status predicted F;161-822/Product: fibroblast growth factor receptor 1, form gamma bl #status pref;171-212/Domain: immunoglobulin homology <IMM>
F;377-397/Domain: intracellular #status predicted <IMM>
F;377-397/Domain: intracellular #status predicted <INT>
F;388-822/Domain: intracellular #status predicted <INT>
F;384-492/Region: protein kinase APP-binding motif F;644-492/Region: protein kinase APP-binding motif F;55-10,178-230,277-341/Disulfide bonds: #status predicted (As) (covalent) #status predicted F;614,511,623/Active site: Lys, Glu, Asp #status predicted F;614,511,623/Active site: Lys, Glu, Asp #status predicted F;628,641/Binding site: magnesium (Asn, Asp) #status predicted F;628,641/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted F;654/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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NiAtternate names: basic fibroblast growth factor receptor
NiContains: protein-tyrosine kinase (EC 2.7.1.112) filg
C;Species: Mus musculus (house mouse)
C;Date: 3.1-06-1933 #text_change 09-Jul-2004
C;Date: 3.1-06-1933 #text_change 09-Jul-2004
C;Accession: A34849; B34849; S09953; A35794; A43025; PC2277
R;Reid, H.H.; Wilks, A.F.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 87, 1596-1600, 1990
A;Title: Two forms of the basic fibroblast growth factor receptor-like mRNA are expresse
A;Reference number: A34849; MUID:90160373; PMID:1689490
A;Accession: A34849
A;Accession: B3484
A;Residues: 1.802 < REI>
A;Cross-references: UNIPROT:P16092; GB:M28998; NID:g192164; PIDN:AAA37290.1; PID:g309116
A;Accession: B3484
A;Residues: 1.30, 120-822 < REZ>
A;Accession: B3484
A;Residues: 1.30, 120-822 < REZ>
A;Accession: B3484
A;Cross-references: GB:M3899
A;Cross-references: GB:M38998
A;Cross-references: GB:M38998
A;Accession: S09933
A;Accessi
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A;Cross-references: GB:M33760
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A;Reference number: A43025
A;Accession: A43025
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636 VMKIADF 642
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Query Match

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C; Species: Homo sapiens (man)
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C; Accession: A55081
R; Dell, KR.; Williams, L.T.
J. Biol. Chem. 267, 21225-21229, 1992
A; Title: A novel form of fibroblast growth factor receptor 2. Alternative splicing of th A; Reference number: A45081; MUID:93016048; PMID:1400433
A; Accession: A45081
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A; Molecule type: nucleic acid
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A; Residues: 1-822 ABL>
A; Cross-references: UNIRNOT:P21802; GB:M97193; NID:9182566; PIDN:AAA52449.1; PID:9182567
A; Residues: Date acid from NCBI backbone (NCBIP:116207)
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology <IMM>
C; Superfamily: basic fibroblast growth factor receptor; F; 172-233/Domain: immunoglobulin homology <IMM>
F; 379-399/Domain: transmembrane #status predicted <TMM>
F; 488-456/Region: protein kinase APP-binding motif F; 488-456/Region: protein kinase APP-binding motif F; 62-107, 179-231, 278-340/Disulfide bonds: #status predicted
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Search completed: June 13, 2005, 14:01:46 Job time : 28 secs

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                                                                                                     June 13, 2005, 13:23:36 ; Search time 113 Seconds (without alignments) 31.722 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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Q74116 mycobacteri Q91687 salmonella Q8x717 escherichia Q8x717 escherichia Q859e0 pseudomonas Q8ty74 methanopyru Q77k59 treponema d Q73k99 treponema d Q63000 rattus norv Q8wmp3 equus cabal Q61153 picrophilus Q89xn0 bradvrhizob	Q99568 gallus gall Q99568 gallus gall Q28152 archaeoglob Q79414 anopheles g Q98bm6 rhizobium l Q9fhy3 arabidopsis Q7807 bos taurus Q28111 bos taurus Q28132 callithrix Q9n0k5 sus scrofa Q6945 oryza sariv Q9ceul lactococcus Q9f4d2 bacteroides	QBU/990 Carva porce QBU/985 agrobacteri Q02529 oryzias lat Q05259 oryzias lat QB1176 oryzias lat QB5717 oryza sativ Q65719 oryza sativ Q65719 oryza sativ QB6711 oryza sativ QB6719 oryza sativ QB6719 oryza sativ QB6719 oryza sativ QB167 descherichia QB167 descherichia QB167 descherichia QB167 morpheles g QB177 methanopyru QB6717 methanopyru QG5056 oryza sativ	QC2016 agrobacteri QB012 bradyrhizob QB012 bradyrhizob QB013 bradyrhizob QB013 corynebacte QB0813 corynebacte QP010 campylobact QP078 saccharomyc QP078 saccharomyc QP078 saccharomyc QP086 myrilus edu QB084 pseudomonas QB084 pseudomonas QB084 corynebacte QB084 corynebacte QB084 archaeoglob PS088 myrilus edu QB087 corynebacte QB087 archaeoglob PS088 archaeoglob PS088 myrilus edu QB085 myrilus edu QB085 myrilus edu QB085 myrilus edu QB085 myrilus edu QB085 myrilus edu QC153 methanococc Quani drosophila QC153 methanococc Q9uani drosophila QS139 mus musculu Q7rry homo sapien Q645x0 homo sapien Q645x0 homo sapien Q645x1 leptospiril Q8089 stranthizob Q908w3 branchiosto Q908w3 branchiosto Q908w4 eptatretus
3 79.3 102 2 79.3 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2 105 2	79.33 79.33 79.33 79.33 79.33 1154 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 1157 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33 79.33	7933 7933 7933 7933 7933 7933 7933 7933	23 79.3 206 2 Q02036 23 79.3 209 2 Q7CXIS 23 79.3 201 2 Q89LZ9 23 79.3 201 2 Q89LZ9 23 79.3 244 2 Q8FX3 23 79.3 244 2 Q7FW14 23 79.3 244 2 Q7FW14 23 79.3 249 1 AQP_AEDAE 23 79.3 249 1 AQP_AEDAE 23 79.3 254 1 PAM_YEAST 23 79.3 254 2 Q70D76 23 79.3 254 2 Q70D76 23 79.3 254 2 Q70D76 23 79.3 254 2 QRARY 23 79.3 201 1 RL2Z_DROME 23 79.3 302 2 Q66SRS 23 79.3 312 2 Q64SX0 23 79.3 312 2 Q64SX0 23 79.3 314 2 Q7TXP8 23 79.3 312 2 Q7TXP8 23 79.3 312 2 Q7TXP8 23 79.3 313 2 Q8HQVI 23 79.3 33 2 Q9UBW4 23 79.3 333 2 Q9UBW4 23 79.3 333 2 Q9UBW4

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Iacono-Connors L.C., Schmaljohn C.S.;
"Cloning and sequence analysis of the genes encoding the nonstructural proteins of Langat virus and comparative analysis with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-FB2-1994 (Rel. 28, Last sequence update)
25-CCT-2004 (Rel. 45, Last sequence update)
Genome polyprotein (Contains: Capsid protein C (Core protein); Matrix
protein (Envelope protein M); Major envelope protein E; Nonstructural
proteins NS1, NS2A, NS2B, NS2A, NS2B, NS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -Xbb bonds in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flaviviruses.";
Virology 188:875-880(1992).

-!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic, supersting a possible membrane-related function. NS5 may play a role in the viral RNA replication. NS3 and NS2B form a protease which processes the viral polyprotein into separate proteins.

-!- CATALYTIC ACTIVITY: Selective hydrolysis of Xaa-Xaa-|-Xbb bonds is which each of the Xaa can be either Arg or Lys and Xbb can be either Ser or Ala.
                                                                                                                                                                                                                                                                                                  Gaps
                    potassium transporters capable of controlling K homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence of the genes encoding the structural proteins of the low-
virulence tick-borne flaviviruses Langat TP21 and Yelantsev.";
Virology 185:891-895(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uangat virus (strain TP21).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RNA)(N).
SUBUNIT: The virion of this virus is a nucleocapsid covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-776 FROM N.A.
MEDLINE-52074260; PubMed-1720591;
Mandl C.W., Iacono-Connors L., Wallner G., Holzmann H., Kunz C.,
Heinz F.X.;
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                           Length 776;
                                                                EMBL; AJ299422; CAC39168.1; --
EMBL; AJ299422; CAC39168.1; --
GO; GO:00106202; Cancembrane; IEA.
GO; GO:0015079; F:potassium ion transporter activity; IEA.
GO; GO:0015079; F:potassium ion transport; IEA.
InterPro; IPR003855; K+ transporter.
Pfam; PF02705; K trans; 1.
TIGRFAMS; TIGR00794; kup; 1.
                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                           Score 28; DB 2;
Pred. No. 1e+02;
0; Mismatches
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0
  Regan S., Fromm J., Hedrich R.;
"Poplar potessium transporters of
and K -dependent xylogenesis.";
Plant J. 32:997-1009(2002).
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                                                                                                                                                                                                                                                             96.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus (strain TP21)
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               604 VMSVAEF 610
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NCBL_TaxID=47664;
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MEDLINE=22381938; Pubmed=12492841;
Langer K., Ache P., Geiger D., Stinzing A., Arend M., Wind C.,
Q73rj6
Q63qb7
Q8yfy0
Q6tvz8
                                                                            Q6tv86
Q6tv18
Q7xc30
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08dbn7
06kic4
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Q91147
Q8cfk8
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Q60830
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Q9qzm7
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Last sequence update)
Last annotation update)
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0974346
099604
NTP1_MXVL
NTP1_SFVKA
063709
089709
07P847
07P847
07P847
07P847
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SYR DEIRA
Q9A9F7
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Q7M182
Q979W1
Q95N25
Q8TH08
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Q8ZPF0
Q7N1L4
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Q8IXC7
Q90330
Q86YI4
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Q8CFK8
Q91150
Q60830
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Q63710
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52TM6
                    Q63QB7
Q8YFY0
Q6TVZ8
Q6TVB6
Q6TVL8
Q7XC30
Q9AY42
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Q8PLP7
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01-DEC-2001
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  Q941L7
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RESULT 1 Q941L7

09730329-60ed.rup

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InterPro; IPRU01850; Helicase C.

R InterPro; IPRU01850; Peptidase S7.

BR InterPro; IPR001851; RNA pol DS PS.

InterPro; IPR007094; RNA pol DS PS.

InterPro; IPR007094; RNA pol DS PS.

InterPro; IPR002877; RRMDFtsd mtfrase.

BR Ffam; PP01009; Flavi alycoprot; 1.

R Ffam; PP01009; Flavi M32, 1.

BR Ffam; PP01009; Flavi M32, 1.

BR Ffam; PP01005; Flavi M32, 1.

BR Ffam; PP01005; Flavi M34, 1.

BR Ffam; PP01005; Flavi M34, 1.

BR Ffam; PP01350; Flavi M34, 1.

BR Ffam; PP01350; Flavi M34, 1.

BR Ffam; PP01290; Flavi M34, 1.

BR Ffam; PP0129; Flavi M34, 1.

BR Ffam; PP0129; Flavi M34, 1.

BR Ffam; PP00121; Havi M54, 1.

BR Ffam; PP00129; Flavi M34, 1.

BR Ffam; PP00121; Havi M54, 1.

BR Ffam; PF00124; Flavi M54, 1.

BR Ffam; PF00149; Flavi M54, 1.

BR Ffam; PP0004; PP014086; Flavi M54, 1.

BR Ffam; PP0004; DRAH M1056; Flavi M54, 1.

BR Ffam; PP0004; DRAH M1056; Flavi M51, 1.

BR PRODOM; PD001456; Flavi M51, 1.

BR PRODOM; PD001456; Flavi M51, 1.

RT PADOM; PD001496; Flavi M51, 1.

BR PRODOM; PD001456; Flavi M51, 1.

BR PRODOM; PD001456; Flavi M51, 1.

BR PRODOM; PD001456; Flavi M51, 1.

BR PRODOM; PM001496; Flavi M51, 1.

BR PRODOM;
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nonstructural protein NS4B (Potential).
RNA-directed RNA polymerase (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Envelope protein M (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1 (Potential).
Nonstructural protein NS2A (Potential).
Flavivirin protease subunit NS2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Removed from capsid protein C by the cellular aminopeptidase.
Capsid protein C (Potential).
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(By similarity).
(By similarity).
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Potential.
Potential.
                                                                                                                                                                                                EMBL; M73835; AAA02740.1; ALT_TERM.
EMBL; S35365; AAB22165.1; -.
PIR; A42545; A42545.
HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000208; Flavi_NS5.
InterPro; IPR002535; Flavi_propep.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS5.
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"Infectious cDNA clones of Langat tick-borne flavivirus that differ from their parent in peripheral neurovirulence.";
virology 269:225-237(2000).
BMBL; AP253420; AAF75260.1; -.
HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . ) (Potential).
N-linked (GlcNAc. . ) (Potential).
N-linked (GlcNAc. . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSPF, H14346, 128'B.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008026; F:ATP-dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003724; F:RNA binding; IEA.

GO; GO:0003724; F:RNA helicase activity; IEA.

GO; GO:0003729; Flavi NS2B.

RILCEPPO; IPRO00529; Flavi NS4B.

RILCEPPO; IPRO00529; Flavi NS4B.
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STRAIN=attenuated strain E5;
MEDLINE=20192178; PubMed=10725214; DOI=10.1006/viro.2000.0220;
                                                                                                                                                                   Score 28; DB 1; Length 3414;
Pred. No. 4.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                        091G39;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         PRT; 3414 AA.
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RNA pol PSvir.
RrmJFtsJ mtfrase.
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PF00869; Flavi_glycoprot; 1.
PF02832; Flavi_glycop_C; 1.
                                                                                                                                                                    96.68;
                                                                                                                                     378017
                                                                                                                                                                                                       6; Conservative
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 3310
3396
3385
3385
570
618
434
                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein precursor.
Langat virus.
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                                                                                                                                                                                                                                                                      929 VMTVAEF 935
                                                                                                                                       3414 AA;
                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flavivirus
DISULFID
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DISULFID
CARBOHYD
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Q9IG39
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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nonstructural protein NS4a.
nonstructural protein NS4b.
membrane-associated glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 2; Length 3414;
Pred. No. 4.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD001556; Flavi_glycoprotE; 1.

Probom; PD001496; Plavi_Sly: 1.

SWART; SM00490; HELICC; 1.

SWART; SM00490; HELICC; 1.

ATP-binding; Helicase; Hydrolase; Polyprotein; Signal.

SIGNAL 780 1128 nonstructural protein NS1.

CHAIN 1129 1358 nonstructural protein NS2a.

CHAIN 1359 1489 nonstructural protein NS2a.

CHAIN 1490 2110 nonstructural protein NS2a.

CHAIN 12559 nonstructural protein NS2a.

CHAIN 2111 2259 nonstructural protein NS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonstructural protein NS5.
envelope membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein.
1 96 capsid protein.
3414 AA; 378138 MW; 8DE86A46A0E8F7E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                            Flavi glycoprotB.
Flavi glycoprotB.
Flavi NS1.
Flavi NS2A.
Flavi NS2B.
Flavi NS4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor.
                                                                                                                                                                                                                                                                                                                                                          RNA_pol_PSvi...; RrmJFtsJ_mtfrase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last seq 01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                               Flavi_propep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoprot, 1
                                                                                                                                                                                                                                                                                      PR001650, Helicase
PR001850, Peptidase
                                                                                                                                                                                                                                Flavi_NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   propep; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.6%;
85.7%;
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Pfam; PF01728; FtsJ; 1.
Pfam; PF00271; Helicase_C;
Pfam; PF00949; Peptidase_S7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                       [PR000336; ]
[PR000069; ]
[PR001157; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                              Flavi
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=TP21;
MEDLINE=20192178; PubMed=10725214; DOI=10.1006/viro.2000.0220;
Campbell M.S., Pletnev A.G.;
"Infectious cDMA clones of Langat tick-borne flavivirus that differ "Infectious CDMA clones of Langat tick-borne":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane-associated glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G0:0019028; C:viral capsid; IEA.
G0:0019031; C:viral envelope; IEA.
G0:0019031; C:viral envelope; IEA.
G0:0008524; F:ATP binding; IEA.
G0:0008026; F:ATP-dependent helicase activity; IEA.
G0:0001723; F:RNA binding; IEA.
G0:0003724; F:RNA helicase activity; IEA.
G0:0003968; F:RNA-directed RNA polymerase activity; IEA.
G0:0003199; F:Structural molecule activity; IEA.
G0:00019079; P:viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3414;
                                                                                                                                                                                                                                                                                                                                                                                            nonstructural protein NS1.
nonstructural protein NS2a.
nonstructural protein NS2D.
nonstructural protein NS3.
nonstructural protein NS4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein NS5.
envelope membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein.
96 capsid protein.
378018 MW; BF8F8ACEAB96D534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                             Probom; PD001556; Flavi_GlycoprotE; 1.
Probom; PD001496; Flavi_NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
ATP-binding; Helicase; Hydrolase; Polyprotein; Signal.
SIGNAL
780 116 Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from their parent in peripheral neurovirulence.";
Virology 269:225-237(2000)
EMBL; AF253419; AR7F5259.1; -.
PIR; B41704; B41704.
HSSP; P14336; ISVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 2; I
Pred. No. 4.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 3414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor.
Pfam; PF01002; Flavi NS2B; 1.
Pfam; PF011350; Flavi NS4A; 1.
Pfam; PF01349; Flavi NS4B; 1.
Pfam; PF01972; Plavi NS5; 1.
Pfam; PF01728; Flavi Dropep; 1.
Pfam; PF001728; FfsJ; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00241; Helicase C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.7
Matches 6; Conservative
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Langat virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3414 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11085;
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Wed Jun 15 09:21:21 2005

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Page 6
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SEQUENCE FROM N.A.

STRAIN=CV. Columbia;

MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;

MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;

MAPER K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

A Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Reis M., Delseny M., Puigdomench P., Watson M., Schmidtheini T.,

Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

Nos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Nan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

Bracken M., Wellighns I., Vote M., Bastiaens I., Aert R., Defoor E.,

Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

Nooijman P., Klein Lankhorst R., Rose M., Hauf J., Wan den Daele H.,

Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

Rottett A., Rajandream M.A., Lynpe M., Benes V., Rechmann S.,

Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FE30; O22399; Q9SUR2; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Potassium transporter 3 (ArPOT3) (AtKUP4) (AtKT3) (Tiny root hair 1
                                                                                                                                             Supervolation of the property 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=POT3; Synonyms=KT3, KUP4, TRH1; OrderedLocusNames=At4g23640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
BEDLINE-21096391; PubMed=11158535;
Rigas S., Debrosses G., Haralampidis K., Vicente-Agullo F.,
Feldmann K.A., Grabov A., Dolan L., Hatzopoulos P.;
"TRH1 encodes a potassium transporter required for tip growth in
Arabidopsis root hairs";
Plant Cell 13:139-151(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 2; Length 433;
Pred. No. 1.1e+02;
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                             lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=147425;
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71.4%;
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Guery Match
Best Local Similarity 71.4°,
Best Local Similarity 71.4°,
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29 IMTVAEF 35
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.eib.ch). RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
R. Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
R. Neumann S., Argiriou A., Vitale D., Ligouri R., Piravandi E.,
R. Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
R. Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
R. Gibbons T., Weber N., Vandenboll M., Bargues M., Terol J., Torres A.,
R. Gibbons T., Weber N., Vandenboll M., Bargues M., Taron D., Jesse T.,
R. Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
R. Heijnen D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
R. Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
R. Parnell L., Dedhia N., Gnoj L., Schutz K., Hanng B., Spiegel L.,
R. Schnomking T., Kalicki J., Graves T., Harmon G., Edwards J.,
R. Schneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
R. Schneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
R. Bentley D., Pulton B., Miller N., Scott K., Johnson D.,
R. Kramer J., Fulton L., Mardis B., Dante M., Pepin K., Hillier L.W.,
Nelson J., Spieth J., Rargibels E., Dante M., Pepin K., Hillier L.W.,
R. Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
R. Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
R. Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
R. Saby I K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
R. Schuene and analysis of chromosome 4 of the plant Arabidopsis root hair growth.
-!- SIMILARITY: Belongs to the HAK/KUP transporter (TC 2.A.72) family.
-!- CAUTION: Ref.2 sequences differ from that shown due to erroneous leaves and flowers of mature plants. of seedlings growth. Sze H., Quintero F.J., Blatt M.R.;  $^{\prime}$  "A new family of K+ transporters from Arabidopsis that are conserved STRAIN=cv. Columbia; MEDLINE=98010480; PubMed=9350997; DOI=10.1016/S0014-5793(97)01125-3; recential). -!- TISSUE SPECIFICITY: Detected at very low levels in roots, stems, -i- FUNCTION: High-affinity potassium transporter required for tip growth of root hairs.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membran Maeser P., Thomine S., Schroeder J.I., Ward J.M., Hirschi K., Sze Talke I.N., Amtmann A., Maathuis F.J.M., Sanders D., Harper J.F., Tchieu J., Gribskov M., Persans M.W., Salt D.E., Kim S.A., "Phylogenetic relationships within cation transporter families of Kim E.J., Kwak J.M., Uozumi N., Schroeder J.I.; "AtKUP1: an Arabidopsis gene encoding high-affinity potassium GENE FAMILY, AND NOMENCLATURE. MEDLINE=21392307; PubMed=11500563; DOI=10.1104/pp.126.4.1646; Arabidopsis."; Plant Physiol. 126:1646-1667(2001) TISSUE SPECIFICITY. MEDLINE=98138058; PubMed=9477571; FBBS Lett. 415:206-211(1997). SEQUENCE OF 1-344 FROM N.A. gene model prediction. Plant Cell 10:51-62(1998). Nature 402:769-777(1999). transport activity across phyla."; Guerinot M.L.; (Potential) thaliana

Length 814;

93.18; 71.48;

6350453B857BEBCB CRC64;

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GO; GO:0006813; P:potassium ion transport; IEA
                Pfam; PF02705; K trans; 1.
TIGRFAMS; TIGR00794; kup; 1.
SEQUENCE 814 AA; 91608 MW;
                                                                  Cuery Match
Best Local Similarity 71.4%,
-hes 5; Conservative
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P47296;
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SEQUENCE
                                                                                                                                                                                                                                                 RESULT 8
DEOC_MYCGE
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Spermatophyta, Magnoliophyta, Liliopsida, Cymodoceaceae, Cymodocea.
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MEDLINE=22261168; PubMed=12374296; DOI=10.1023/A:1019951023362;
MEDLINE=22261168; PubMed=12374296; DOI=10.1023/A:1019951023362;
Garciadeblas B., Benito B., Rodriguez-Navarro A.,
"Molecular cloning and functional expression in bacteria of the potassium transporters ChHAK1 and ChHAK2 of the seagrass Cymodocea
                                        EMBL; AL015394; CAA30300.1; ALT_SEQ.
EMBL; AL01559; CAB79319.1; ALT_SEQ.
EMBL; AP012659; AAC49846.1; -.
EMBL; AF012659; AAC49846.1; -.
EMBL; T05596; T05596.
InterPro; IPR003855; K+ transporter.
Pfam; PF02705; K trans; 1.
TIGRPAMS; TIGR00794; kup; 1.
Multigene family; Potassium transport; Transmembrane; Transport.
DOMAIN 1 31 Potential).
TRANSMEM 11 31 Potential.
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EMBL; AJ427293; CAD20319.1; -.
GO; GO:00146070; C:Medagaium ion transporter activity; IEA.
GO; GO:0015079; P:potassium ion transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential) BOCS5068B48E8180 CRC64;
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01-JUN-2003 (TrEMBLrel. 20, Last sequence update)
Putative potassium transporter.
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                  CAC16137.1;
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VMSIAEF 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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-I. CATALYTIC ACTIVITY: 2-deoxy-D-ribose 5-phosphate = D-glyceraldehyde 3-phosphate + acetaldehyde alphosphate + acetaldehyde - application and deoxyribonucleotide catabolism.
-I. SAMELMAN: Nucleotide and deoxyribonucleotide catabolism.
-I. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase)
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schiff-base with acetaldehyde (By aimilarity).
By similarity.
332430231CB99DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 1; Length 223; Pred. No. 1.1e+02;
Score 27; DB 2; Length 814
Pred. No. 2.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                           223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Lyase; Schiff base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=deoC; OrderedLocusNames=MG050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00114; -; 1.
InterPro; IPR002915; DeoC.
InterPro; IPR003009; FMN_enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24675 MW;
                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39684; AAC71266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Deoxyriboaldolase) (DERA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01791; DeoC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152
                                                                                                                                                                            611 VMSIAEF 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; E64205; E64205.
HSSP; O66540; 1MZH.
TIGR; MG050; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
223 AA;
                                                                                                                1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily 1.
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RESULT 9 DEOC_MYCPN

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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016832; F:aldehyde-lyase activity; IEA.
GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                     STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome."; submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. BMBL, AE010267; AL181814.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 2; Length 324;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 2; Length 262;
Pred. No. 1.3e+02;
                                                        01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Town C.D., Kaul S.;
Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AAC006836; AAD20079.1; -.
PIR; B84452; B84452.
HSSP; P52839; 1044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 AA; 29225 MW; ED84D28FD5DEADC2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0008146; F:sulfotransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IPR000863; Sulfotransferase. Pfan; PF00685; Sulfotransfer_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ffam, PF00793; DAHP_synth_1; 1.
TIGRFAMS; TIGR01361; DAHP_synth_Bsub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001218; SulfotransFerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative steroid sulfotransferase.
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 89.7%;
Similarity 71.4%;
5; Conservative 1
                            01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                   OrderedLocusNames=PF1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                  Pyrococcus furiosus
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39 IMKVAEF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 262 AA;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VMXVAEF
                                                                                                                                                                                                                                                                    NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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   ACCOORDING THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase)
(Deoxyriboaldolase) (DERA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loechel S., Inamine J.M., Hu P.-C.; "Nucleotide sequence of the deoC gene of Mycoplasma pneumoniae."; Nucleic Acids Res. 17:801-801(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 24:4420-4449(1996).

-!- CATALYTIC ACTIVITY: 2-deoxy-D-ribose 5-phosphate = D-glyceraldehyde 3-phosphate + acetaldehyde.

-!- PATHWAY: Nucleotide and deoxyribonucleotide catabolism.
-!- SUBCELJULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the deoC/fbaB aldolase family. DeoC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Lyase; Schiff base.
BINDING 152 152 Schiff-base with acetaldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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By similarity.
73C3E4932E7881F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Name-deoC; OrderedLocusNames=MPN063; ORFNames=MP091; Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 1; I
Pred. No. 1.2e+02;
                                                                                                                                                                                  224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=89128453; PubMed=2492658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AA; 24878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13544; CAA31897.1; -.
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71.4%;
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PIR; S02216; S02216.
HSSP; Q9X1P5; 100Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAE; MF 00114; -; 1.
InterPro; IPR002915; DeoC.
Pfam; PF01791; DeoC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
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|| :|||
93 VMNIAEF 99
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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93 VMNIAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae."
                                                                                                                                                                                  MYCPN
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DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.B., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Fraser C.M.
"Complete genome sequence of the oral pathogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderediocusNames=PG0232;
Porphyromonas gingivalis (Bacteroides gingivalis)
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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Pred. No. 3.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                   Similarity 71.4%; Score 26; DB 2; Length 731; Similarity 71.4%; Pred. No. 3.5e+02; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XBW4; Q7BWB5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Immunoreactive 92 kDa antigen PG21 (Zinc carboxypeptidase,
   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hocking D., Webb E.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                        EMBL; AP005102; BAC83706.1; -.
InterPro; IPR007658; DUF594.
Pfam; PF04578; DUF594; 1.
Hypothetical protein:
SEQUENCE 731 AA; 82975 MW; 62C331F04D1716AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     821 AA; 91517 MW; 250843B2C9C833E2 CRC64;
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SMART; SM00089; PKD; 3.
SMART; SM00631; Zn pept; 1.
PROSITE; PS00013; CARBOXYPEPT ZN 2; UNKNOWN 1.
PROSITE; PS50093; PKD; 3.
COMPLETE PSTOCEOME.
SEQUENCE 821 AA; 91517 MW; 250843B2C9C833E
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J. Bacteriol. 185:5591-5601(2003).
EMBL; AR153768; AAD38980.1; -.
EMBL; AR017172; AAQ65462.1; -.
HSSP; Q90240; 1QMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR000834; Peptidase_MI4.
InterPro; IPR000601; PKD.
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NCBI_TaxID=837;
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Pfam; PF00801; PKD; 3.
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Similarity 85.7%;
6; Conservative
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391 IMGVAEF 397
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TIGR; PG0232; -.
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Best Local Similarity
Matches 6; Conserv
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Matches 5; Conserv
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licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
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Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
   Gaps
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Name=OSJNBa0033J14.4;
Orza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;

"The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein tuaB. Name-tuaB; OkrNames=Bu3350, BLi03806; Bacillus licheniformis DSM 13. Bacteria; Firmicutes; Bacillase; Bacillus
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EMBL; CP000002; AAV25249.1; -.
Hypochetical protein.
SEQUENCE 479 AA; 53318 MW; B25425B96AD39D62 CRC64;
                                                                                                                                                                                                                                                                                                                      25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
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Pred. No. 2.4e+02;
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1; Mismatches
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5; Conservative
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les 4; Conservative
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233 VMRIAEF 239
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                                                           VMXVAEF 7
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STRAIN=168;
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A Atkins T., Crossman L.C., Pitch T., Churcher C., Murgall K.,
A Atkins T., Crossman L.C., Pitch T., Churcher C., Murgall K.,
A Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
A Ketth K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivliai S., Stevens K., Tunapa S., Vesaratchavest M.,
A Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
T. Genomic plasticity of the causative agent of melioidosis,
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                                                                                                                                                                                                                                                                                                           Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.2%; Score 25; DB 2; Length 205; 71.4%; Pred. No. 2e+02;
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SEQUENCE 205 AA; 21152 MW; 67216B40EBF4D59F CRC64;
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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nes 5; Conservative
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                                                          565 VMPVAEF 571
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VLAVAEF 61
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                 VMXVAEF
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25-OCT-2004
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0621K2
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Runst F., Ogasawara N., Mozzer I., Albertini A.M., Alloni G.,

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Ra Azevedo V., Beruschi C., Caldwell B., Capuano V., Carter N.M.,

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Rabenizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Rabenizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Rabenizot F., Claser P., Goffeau A., Golightly B.J., Grandi G.,

Rabenizot F., Glaser P., Goffeau A., Golightly B.J., Grandi G.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

A Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Lepidus A., Golightly B.J., Rabanchard M.,

Rabens L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,

Ranno M., Kurita K., Lepidus A., Lardinois S., Lauber J.,

Ranno M., Kurita K., Lepidus A., Lardinois S., Lauber J.,

Ranno M., Kurita K., Lepidus A., Lardinois S., Lauber J.,

Ranno M., Reynolds S., Rieger M., Mizuno M., Moestl D., Roche B.,

Rap Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,

Rap Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

Rap Resecut A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,

Rap Remaru K., Takenuchi M., Tamakoshi A., Taekagi T., Tarkaji T., Takahashi H.,

Rap Remaru K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,

Mattenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,

A Vasiarotti A., Viari A., Wambutt R., Wedler E., Wedler E., Wedler I. R.,

Rap Yoshikawa H., Danchin A.,

Rap Yoshikawa H., Danchin A.,

Rap Yoshikawa H., Panchin A.,

Rap Yoshikawa H., Pan
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                                                                                                                                                                             Similarity 71.4%; Pred. No. 2e+02; 5, Conservative 1; Mismatches 1; Indels
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Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL; BX571965; CAH35173.1; -.
SEQUENCE 205 AA; 21152 MW; 67216B40EBF4D59F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTBQ_BACSU STANDARD; PRT; 253 AA. P5356; 034914; 01-0CT-1996 (Rel. 34, Created) 01-0CT-2094 (Rel. 34, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Hypothetical protein ytb0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ytb0; OrderedLocusNames=BSU30180;
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MEDLINE=96312354; PubMed=8763940;
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J. Bacteriol. 178:4122-4130(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 VLAVAEF 61
                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
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111 VLSVAEF 117
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SEQUENCE 61
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidase T.
Name-pepT-2; OrderedLocusNames-EF3080;
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
[1]
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the BNBL/GenBank/DDBJ databases.
EMBL; AE010154; AAL80426.1; -...
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
Pfam; PP04055; Radical SAM; 1.
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                                                                                                                                                                                                                                                                                                                          Length 253;
                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                              EMBL, U51868; AAB17463.1; -.
EMBL, AF008220; AAC00267.1; ALT_INIT.
EMBL, 299119; CAB14996.1; ALT_INIT.
Subtinist; BG11787; ytb0.
Complete proteome; Hypothetical protein.
SEQUENCE 253 AA; 28233 MW; 572CC4681F04C650 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                       86.2%; Score 25; DB 1; I
57.1%; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Co-factor modifying protein. OrderedLocusNames=PF0302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21,
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les 4; Conservative
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222 IMKIAEF 228
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75 IMDIAEF 81
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                                                                                                                                                                                                                                                                                                                     Query Match
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Q82ZH7;
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10 081327
AC 081322
AC 08132
DT 01-JU

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Matches
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0822H7
10 0822H AC 0822H AC 0822H DT 01-JU DT 01-JU DT 01-JU DT 01-JU DT 01-MA DS ENTER OS ENTER OS ENTER OS NOBL RN [1]
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STRAIN-V583 / ATCC 700802; MBDLINDEASSEGUECE.1080613; MBDLINBEA2558085; Pubmed=12663927; DOI=10.1126/science.1080613; Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nalson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                           "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.2%; Score 25; DB 2; Length 406; 71.4%; Pred. No. 3.8e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 AA; 44953 MW; 038ABFCD17BA85DE CRC64;
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17 AA; 66569 MW; 20512A41BAC1E599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0008237, F:metallopeptidase activity, IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IRR001261, ArgE dapE.
InterPro; IPR010161; Peptidase_M20B.
PIGRPAMS; TIGR01882; peptidase-T; 1.
PROSITE; PS00758; ARGE_DAPE_CPG2_1; 1.
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GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0051082; F:unfolded protein binding; IEA.
GO; GO:00526; P:iron-sulfur cluster assembly; IEA.
InterPro; IPR010236; HspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chaperone protein HscA.
Name=hscA; OrderedLocusNames=HD1087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                Science 299;2071-2074(2003).
EMBL; AE016956; AA082761.1; -.
HSSP; P29745; 1VIX.
TIGR; EF3080; -.
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ProDom; PD000089; HSP70; 1.
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Best Local Similarity 71.4
Matches 5; Conservative
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METAL
METAL
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Q7UYJ7
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                                                               ö
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Accepts electrons from ETF and reduces ubiguinone (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Reduced electron-transferring flavoprotein ubiquinone = electron-transferring flavoprotein + ubiquinol.
-!- COFACTOR: FAD and a 4Fe-4S cluster (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
                                                                                                                                                                                                                                                                                                         ETFD_SCHPO STANDARD; PRT; 632 AA.

987111,
987111,
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OGT-2004 (Rel. 45, Last annoctation update)
Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.5.5.1) (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (Electron-transferring-flavoprotein dehydrogenase)
0000 (ETF dehydrogenase)
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86.2%; Score 25; DB 2; Length 617; 71.4%; Pred. No. 5.7e+02; ive 1; Mismatches 1; Indels
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-!- SIMILARITY: Belongs to the ETF-QO / fixC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                       553 VLSVAEF 559
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                                                                                                                1 VMXVAEF 7
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EMBL, BX294133; CAD71645.1; -...

GO, GO:0003844; F:1,4-alpha-glucan branching enzyme activity; IEA.

GO, GO:0004556; F:alpha-amylase activity, hydrolyzing O-glycosyl . .; IEA.

GO, GO:0004577; F:transferase activity, transferring glycosyl . .; IEA.

GO, GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR00647; Alpha amyl cat.

InterPro; IPR004193; Glyco_hydro_13N.

InterPro; IPR004193; Glyco_hydro_13N.

Pfam; PF00128; Alpha-amylase, N. 1.

Pfam; PF02922; Isoamylase_N, 1.
                                                                                                                                                                                                                                                                                                          Mitochondrion (Potential).

Probable electron transfer flavoprotein-
ubiquinone oxidoreductase.

FAD (ADP part) (Potential).

Iron-sulfur (4Fe-4S) (Potential).

Iron-sulfur (4Fe-4S) (Potential).

Iron-sulfur (4Fe-4S) (Potential).

Iron-sulfur (4Fe-4S) (Potential).
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                            Interro; Int
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Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 633 AA; 72019 MW; 708ECC306CC9D9E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69472 MW; 1B0F22374E33771B CRC64;
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01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18).
Name-glgB; OrderedLocusNames=RB548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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EMBL, 295334; CAB08598.1; -. PIR, T38126; T38126. GeneDB GeneDB SPAC20G8.04c; InterPro; IPR007859; ETFD.
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5; Conservative
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193 VMSLAEF 199
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Best Local Similarity
Matches 5; Conserv
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FROM N.A.
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P29198;
     SEQUENCE
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RL13_HALMA
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"Structural analysis of the regions of 1,044,062 bp covered by thirteen
I physically assigned Pl clones.";
DNA Res. 4:291-300(1997).

R EMBL; U40566; AAB37569.1; -.

R EMBL; BAB06700; BAB08968.1; -.

R EMBL; BAB06700; BAB08968.1; -.

R GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004839; F:ubiquitin activating enzyme activity; IEA.

GO; GO:000512; P:ubiquitin activating enzyme activity; IEA.

R O; GO:000512; P:ubiquitin activating enzyme activity; IEA.

R InterPro; IPR008026; Lipase AS.

R InterPro; IPR000504; MAD BS.

R InterPro; IPR000105; WAD BS.

R InterPro; IPR000101; UdacE_repeat.

InterPro; IPR00011; Udtin-activ_enz.

R Pfam; PF00899; Thif; 2.

Pfam; PF00899; Thif; 2.
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATPase class II (Fragment)

Bagrus major (Red sea bream) (Chrysophrys major).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Sparitomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
NCBL TaxID=143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
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TIGRFAMS; TIGRO1408; UDe1; 1.
PROSITE; PS00120; LIPASE SER; UNKNOWN 1.
PROSITE; PS00865; UBIQUITIN ACTIVAT 1; 1.
PROSITE; PS00865; UBIQUITIN ACTIVAT 2; 1.
SEQUENCE 1077 AA; 119622 WW; CE39A36AAA99A218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAALB-ecotype Columbia;
Hatfield P.M., Carpenter T.C., Vierstra R.D.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                   PRT; 1077 AA.
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                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                     Ubiquitin activating enzyme 2
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                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03,
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                                                                                                   PRELIMINARY;
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VMSMAEF 60
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Matches 5; Conserv
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STRAIN=ATCC 43049;
MEDLINE=20396344; PubMed=10937989; DOI=10.1126/science.289.5481.905;
Ban N., Nissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at 2.4 A resolution.";
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"A pre-translocational intermediate in protein synthesis observed in crystals of enzymatically active 508 subunits.";
Nat. Struct. Biol. 9:225-230(2002).
                                                                                                                                                                                                                                                                                                                                           Gaps
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TISSUE-Spleen;
Chen S.L., Xu M.Y., Hu S.L., Li L.;
"Analysis of immune-relevant genes expressed in red sea bream
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"Halobacterial S9 operon. Three ribosomal protein genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cotranscribed with genes encoding a tRNA(Leu), the enclase, putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 41049;
bubMed=10031990; DOI=10.1126/science.289.5481.920;
Nissen P., Hansen J., Ban N., Moore P.B., Steitz T.A.;
"The structural basis of ribosome activity in peptide bond
                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                                                                                                                                           Score 24; DB 2; Length 140;
Pred. No. 2.76+02;
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PubMed=11483524; DOI=10.1093/emboj/20.15.4214;
Klein D.J., Schmeing T.M., Moore P.B., Steitz T.A.;
"The kink-turn: a new RNA secondary structure motif.";
EMBO J. 20:4214-4221(2001).
                                                                                                                                                                                                               SEQUENCE 140 AA; 15723 MW; 20EFF0F49C40EB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 145 AA
                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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PubMed=11828326; DOI=10.1038/nsb758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92105119; Pubmed=1840597;
                                                                                                                     Aquaculture 240:115-130(2004).
EMBL; AY190684; AAP20160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacteriaceae; Haloarcula.
                                                                                                                                                                                                                                                                        h 82.8%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 289:905-920(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 LMVVAEF 78
                                                                                                                                                                                                                                                                                                                                                                                                     1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=rpl13p;
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X-RAY

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MEDLINE=21929760; PubMed=1193228; DOI=10.1101/gr.223902; MEDLINE=21929760; PubMed=1193228; DOI=10.1101/gr.223902; Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvos S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PubMed=15064768,
Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,
Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R.,
Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
"The genome sequence of the extreme thermophile Thermus
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Archaea, Buryarchaeota, Methanomicrobia, Methanosarcinales;
Methanosarcinaceae, Methanosarcina.
3D-structure; Ribosomal protein; RNA-binding; rRNA-binding. SEQUENCE 145 AA; 16228 MW; 069CE666662AE3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 71.4%; Pred. No. 2.8e+02; Similarity 71.4%; Pred. No. 2.8e+02; S; Conservative 1; Mismatches 1; Indels
                                                                          82.8%; Score 24; DB 1; Length 145; 83.3%; Pred. No. 2.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE017304; AAS81457.1; -
Interpro; IPR009072; Histone-fold.
Complete proteome; Hypothetical protein.
SEQUENCE 148 AA; 16860 MW; 0AA40838B46F96AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                          072IL7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein
OrderedLocusNames=TTC1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MA2884.
OrderedLocusNames=MA2884;
                                                                                                                                                                                                                                                                                                                                                        148 AA.
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Biotechnol. 22:547-553 (2004).
                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                 Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                             2 MXVAEF 7
                                                                                                                                                                                                                           1 MSVAEF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermophilus."
                                                                               Query Match
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Q721L7
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PubMed=1456184; DOI=10.1261/rna.5120503;
Schmeing T.M., Moor=10.8 Steitz T.A.;
Schmeing G. Geacylated tRNA mimics bound to the E site of the large "Structures of deacylated tRNA mimics bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA 9:1345-1352(2003).
-!- FUNCTION: Binds to the 238 rRNA.
-!- SUBUNIT: Part of the 508 ribosomal subunit. Interacts weakly with proteins L3 and L6.
-!- SIMILARITY: Belongs to the ribosomal protein L13P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF THE 50S SUBUNIT IN COMPLEX WITH FIVE ANTIBIOTICS AT THE PEPTIDYL TRANSFERASE CENTER. STRAIN=ATCC 43049;
                            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF THE 50S SUBUNIT IN COMPLEX WITH FOUR MACROLIDE ANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen J.L., Moore P.B., Steitz T.A.;
"Structures of five antibiotics bound at the peptidyl transferase center of the large ribosomal subunit.";
J. Mol. Biol. 330:1061-1075(2003).
                                                                                                                                                                             "The structures of four macrolide antibiotics bound to the large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF THE 50S SUBUNIT WITH
                                                                                                   PubMed=12150912; DOI=10.1016/S1097-2765(02)00570-1;
Hansen J.L., Ippolito J.A., Ban N., Nissen P., Moore P.B.
                                                                                                                                                                                                                                                                              CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF THE 50S SUBUNIT.
                                                                                                                                                                                                                                                                                                                          PubMed=12185246; DOI=10.1073/pnas.172404099; Hansen J.L., Schmeing T.M., Moore P.B., Steitz T.A.; "Structural insights into peptide bond formation."; Proc. Natl. Acad. Sci. U.S.A. 99:11670-11675(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12860128; DOI=10.1016/S0022-2836(03)00668-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1086; X-ray; K=1-145.
PDB; 10VF; X-ray; I=1-145.
PDB; 10VG; X-ray; I=1-145.
INTERPRO; IPRO05822; Ribosomal L13.
INTERPRO; IPRO05755; Ribosomal L13.
ProDom; PO00179; Ribosomal L13; I.
ProDom; P000179; Ribosomal L13; I.
ProDom; P000179; Ribosomal L13; I.
PROSITE; PS00783; RIBOSOMAL L13; 1.
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                                                                                                                                                                                                    ribosomal subunit.";
Mol. Cell 10:117-128(2002)
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107Y; X-ray; K
1081; X-ray; K
1082; X-ray; K
                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 43049;
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1KC8; X-ray;
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1KQS; X-ray;
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                                                                                                                                                      Steitz T.A.;
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1N8R;
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriquchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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DNA Res. 9:189-197(2002).
EMBL; AP005958; BAC51792.1; -.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 1; Length 157;
Pred. No. 3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 24; DB 2; Length 161; 71.4%; Pred. No. 3e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                 Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000531; Bet v I; 1.
PROSTIE; PS00451; PATHOGENESIS BETVI; 1.
Allergen; Pathogenesis relaced protein; Plant defense.
SEQUENCE IS7 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 AA; 17456 MW; 4B7895C4BF28D199 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
B116527 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF036931; AAB92255.1; -.
HSSP; O24248; 1E09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000916; Bet v I. Pfam; PF00407; Bet v I; I. PRINTS; PR00634; BETALLERGEN.
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VMXVAEF 7
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              NCBI_TaxID=50225;
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SEQUENCE 161 AA
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                  SO WE WAS A STANCE OF THE STAN
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30-MAY-2000 (Rel. 39, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
29-MAR-2004 (Rel. 43, Last annotation update)
Root allergen protein (RAP).
Taraxacum officinale (Common dandelion).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander B., Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

Genome Res. 12:532-542(2002).

Golowe Res. 12:532-542(2002).

GO, GO:0008168; F:methyltransferase activity; IEA.
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
NCBI_TaxID=182099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 2; Length 149;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             149 AA; 16402 MW; EF8576A410EC13F3 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last amnotation update)
Putative succinyl-CoA synthase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AA
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MEDLINE=22505401; PubMed=12618405;
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Pfam; PF02629; Coa binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 149 AA;
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049065;
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10862D3
AC 0862D4
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Matches
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Gaps

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Q6AQI2;

RESULT 31
006AQ12
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                    Gaps
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Proc. Matl. Acad. Sci. U.S.A. 100:8298-8303 (2003).

-1- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                       PS9932; QTUKV3;
9-9MR-2004 (Rel. 43, Created)
29-MR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
8-JUL-2004 (Rel. 46) Last annotation update)
8-JUL-2004 (Rel. 47) Restand binding protein (SSB) (Helix-destabilizing protein).
Name-ssb; OrderedLocusNames=RB9917;
Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=1;
MBDLINB=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
MBDLINB=2735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
Glockner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
Schlesner H., Amann R., Reinhardt R.;
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                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
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InterPro, IPR010913; SS_binding.
InterPro, IPR000424; SSB_protein.
Pfam, PF00436; SSB, 1.
TIGREPMS; TIGR06SSB; 1.
PROSITE; PS50935; SSB; 1.
COMPLETE proteome; DNA repair; DNA replication; DNA-binding.
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83.3%; Pred. No. 3.2e+02;
iive 0; Mismatches 1; Indels
                    Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Multisubunit N+/H+ antiporter, subunit E.
Name=mrpB; OrderedLocusNames=cg3027;
71.4%; Pred. No. 3.1e+02;
tive 1; Mismatches 1;
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Matches 5; Conservative
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                                                                                                         107 VLLVAEF 113
  Best Local Similarity
                                                                1 VMXVAEF 7
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                                                                                                                                                                            RESULT 33
SSB_RHOBA
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";
Environ. Microbiol. 6:887-902 (2004).
EMBL: CF522870, CAG35391.1; -.
INTERPRO: IPR009921; DUF1456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                        Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R., Klenk H.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=GB-M1;
BDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                   Desulfotalea psychrophila.
Bacteria, Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
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Encephalitozoon cuniculi GB-M1.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NGBI_TaxID=284813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 2; Length 162; 57.1%; Pred. No. 3e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 24; DB 2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ALS90448; CAD26373.1; -. 60; GO:0006810; P:transport; ITA. InterPro; IPR011012; Longin like. SEQUENCE 165 AA; 18742 MW; 7CDAB6C35BC11A6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA; 19034 MW; 5E67041F45744728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
COATOMER ZETA SUBUNIT.
                                                                                                              Last sequence update)
Last annotation update)
                                             162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AA
                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                             PRT;
                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 44)pochetical protein. OrderedLocusNames=DP0662;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=LSv54 / DSM 12343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.1 Matches 4; Conservative
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|:|||
114 IMALAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      PubMed=15305914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope;
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Query Match

Q8SRD1

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RESULT 32
085RD1
AC 085RD
AC 085RD
DT 01-JUU
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Query Match

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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=2139325; PubMed=11466286;

MEDLINE=2139325; PubMed=11466286;

MODI=10.1128/JB.183.16.4823-4838.2001;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Baly M.J., Bennett G.N., Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-483812001.

-I. CATALYTIC ACTIVITY: ATP + thymidine = ADP + thymidine 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 2; Length 189; 71.4%; Pred. No. 3.5e+02; rive 0; Mismatches 2; Indels
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--- SIMILARITY: Belongs to the thymidine kinase family.

REMEL, ABC07786; AAK80830.1; ---
PIR: C97255; C97255.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016301; F:Kinase activity; IEA.

GO; GO:0016797; F:Lymidine kinase activity; IEA.

GO; GO:0016797; F:Lymidine kinase activity; IEA.

GO; GO:0016797; F:Lransferase activity; IEA.

RO; GO:0016259; P:DNA metabolism; IEA.

RILERPRO; IPR000345; CytC heme_BS.

RILERPRO; IPR001267; TK_Cell.
                                                                                                                                                                                                                                                                                                                                      WormBags, WEGENERO, TO THE STATE STA
                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AC024200; AAF35997.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0089; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 189 AA; 21048 MW; 7BDA2D05F0362CD0 CRC64;
                                                                                      Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00265; TK; 1. __PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thymidine kinase.
OrderedLocusNames=CAC2887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                        WormBase Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 VMTAAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                          Q9LRB7; 11YM
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                                   STRAIN=Bristol N2;
  SEQUENCE FROM N.A.
                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1488;
                                                              Wilson R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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        셤
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                                                                                                                                   SEQUENCE FROM N.A.
STRAIR=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Ralinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaiglat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                  "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins."; 0. Biotechnol. 104:5-25(2003).

EMBL; BX927156; CAF20754.1; -- GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0008324; F:cation transporter activity; IEA.

GO; GO:0006812; P:cation transport; IEA.
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 2; Length 169;
Pred. No. 3.2e+02;
1; Mismatches 1; Indels
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Bradshaw-Cordum H., Scott K., Graves T.;
"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wilson R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19166 MW; CB9AA69662E22A36 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-CT-2000 (TrEMBLrel. 15, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annoi
Hypotherical protein Y11F9AL.10.
Name=Y71F9AL.10, ORFNames=Y71F9AL.10;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR002758, Cation_antiport.
ProDom, PD012569, DUF68, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.43,
Best Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2002)
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VMLMAEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 AA;
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Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                      NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                                                          rauch A.;
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RESULT 35
090411
AC 09041
DT 01-MA
DE HYPOTO
CACODO

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Gaps

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TIGR; MT2635;
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YP88_MYCBO
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MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Elglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GMI1000;

K MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

A Azlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Azlat M., Elilault A., Brottier P., Camus J.C., Cattolico L.,

Chandler M., Choisne N., Claudel-Renard C., Curnac S., Demange N.,

A Gaspin C., Lavie M., Moisan A.; Robert C., Saurin W., Schiex T.,

Signier P., Thebault P., Whalen M., Wincker P., Levy M.,

Meissenbach J., Boucher C.A.;

I "Genome sequence of the plant pathogen Ralstonia solanacearum.";

I "Genome sequence of the plant pathogen Ralstonia solanacearum.";

EMBL; AL646070; CAD16174.1;

EMBL; AL646070; CAD16174.1;

Complete proteome; Transmembrane.

SEQUENCE 206 AA; 21783 MW; 8D49E45AISOB8440 CRC64;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
PROSITE; PS00603; TK_CELJULAR_TYPE; UNKNOWN 1.
ATP-binding; Complete proteome; DNA synthesis; Kinase; Transferase.
SEQUENCE 195 AA; 22303 MW; 6EDB551986B203BA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%; Score 24; DB 2; Length 206; 57.1%; Pred. No. 3.8e+02; tive 2; Mismatches 1; Indels
                                                                                                  Length 195;
                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=Rv2558, MT2635; ORFNames=MTCY9C4.10c;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PRODABLE TRANSMEMBRANE PROTEIN.
Name-RS011138; OrderedLocusNames-RSC2467;
                                                                                                Match 82.8%; Score 24; DB 2; I Local Similarity 57.1%; Pred. No. 3.6e+02; es 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPS8 MYCTU STANDARD; PRT; 236 AA. P65005; Q50740; 01-NOV-1997 (Rel. 35, Created) 25-0CT-2004 (Rel. 45, Last sequence update) 25-0AN-2005 (Rel. 46, Last annotation update) Hypothetical protein Rv2558/MTZ635.
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                            131 LMAIAEF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 VLAIAEF 61
                                                                                                                                                                                              1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=305;
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                                                                                                  Query Match
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                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                    RESULT 37
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=2206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2557.
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:837-844 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=AF2122/97; PubMed=12788972; DOI=10,1073/pnas,1130426100; MEDLINE=22709107; PubMed=12788972; DOI=10,1073/pnas,1130426100;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 1; Length 236;
Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; Rv2558; -.
Interpro; IRR011008; Inmer A_B barrel.
Complete proteome; Hypothetical protein.
SEQUENCE 236 AA; 25718 MW; 13E3B049D8F79C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P65006; Q50740;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Pypothetical protein MD5588.
OrderedLocusNames=MD2588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BX842580; CAB01046.1; -. EMBL; AE000516; AAK46947.1; -. PIR; B70728; B70728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 82.8%;
Similarity 71.4%;
5; Conservative 1
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Best Local Similarity
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STRAIN=MoPn / Nigg;
MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
MCClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                              Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                      Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D., Stajandream M.A., Barrell B.G., Submitted (BPR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL139794; CAC22635.1; -. Hypothetical Tribals.
Hypothetical protein.
SEQUENCE 248 AA, 26365 MW; A80440E18B3F69B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                             "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
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Similarity 71.4%; Score 24; DB 2; Length 248
Similarity 71.4%; Pred. No. 4.6e+02;
5; Conservative 1; Mismatches 1; Indels
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01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Serine/threonine protein phosphatase, putative.
                                                                                                                                                                                                                                   Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR001932; PP2C-like.
Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 28.1397-1406(2000).
EMBL; AE002321; AAF39372.1; -.
PIR; G81693; G81693.
                                                                                                                                                                                            STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
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Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 LMRVAEF 202
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                         NCBI TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Friedlin;
                                                         Name=L7610.05;
                                                                                                                                                                                                                                                          Smith D.F.;
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MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.,
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI TaxID=1717;
                                                                                                                                                                                                                                                                                                                      82.8%; Score 24; DB 1; Length 236; 71.4%; Pred. No. 4.3e+02; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                     EMBL; BX248343; CAD94773.1; -.
InterPro; IPR011008; Dimer A B barrel.
Complete proteome; Hypotherical protein.
SEQUENCE 236 AA; 25718 MW; 13E38049D8F79C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Hypothetical protein.
SEQUENCE 238 AA; 24945 MW; 1560BB577A2194F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphtheriae NCTC13129.";
Nucleic Acids Res. 31.6516.6523(2003).
BM248356; CAR54935.1;
GO, GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0005608; P:proteolysis and peptidolysis; IEA.
InterPro; IPR012886; Peptidase M238.
InterPro; IPR011054; Rudmnt hyb.motif.
PF01551; Peptidase M23; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=DIP0836;
                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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VLSIAEF 78
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RESULT 41 097008 ID 09700 AC 09700 DT 01-MA DT 01-MA

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
(Phosphohoxokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moduray A.A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 292839; CAB07417.2; -
Wormbase; WEGNE00011607; T08D2.2.
Wormpase; WEGNE00011607; T08D2.2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0003834; F:catalytic activity; IEA.
GO; GO:000629; P:lipid metabolism; IEA.
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 317 AA; 36591 MW; 145E88B02B75AE42 CRC64;
                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T08D2.2.
ORFNames=T08D2.2;
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                                                                                                                                                                                                                           317 AA.
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  Mismatches
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InterPro; IPR000715; Glyco_trans_4.
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box; 1. Pfam; PF00953; Glycos transf 4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998)
4; Conservative
                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
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244 VMSIAEY 250
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                                                   1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                    Q9U375;
01-MAY-2000
01-MAY-2000
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01-0CT-2003 (TrEWBLrel. 25, Last annotation update)
Hypothetical protein L5075.02.
Name=L5075.02;
Leishmania major.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=290434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Friedlin;
MEDLINE=98146435; PubWed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRAIN-EB;

A Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
A Schulte-Spechtel U., Wilske B., Suchnel J., Platzer M.;
"Comparative analysis of the Borrelia garinii genome.";
"Comparative analysis of the Borrelia garinii genome.";
"Comparative analysis of the EMEL/GenBank/DDBJ databases.
E Submitted (JUN-2004) to the EMEL/GenBank/DDBJ databases.
R GO; GO:0016140; Fracyltransferase activity; IEA.
R GO; GO:0016740; Frtransferase activity; IEA.
R GO; GO:0016740; Frtransferase activity; IEA.
R GO; GO:0016740; Frtransferase.
R GO; GO:0016740; Transferase.
R GO; GO:0016740; Transferase.
R GO; GO:0016740; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 2; Length 270; 71.4%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck A., Klages S., Reinhardt R., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, All63552 and All63552 protein. Fypochetical protein. SEQUENCE 270 AA; 29335 MW; 5B91DA37Al6FC3CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Glycerol-3-phosphate O-acyltransferase, putative. ORFNames=BG0328;
                                                                                                                                                                               270 AA
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les 5; Conservative
                                                                                                                                                                            PRELIMINARY;
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148 VMNLAEF 154
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Best Local Similarity
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                                                                                                                   RESULT 43
Q9NE74
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP, MF 00339; -; 1.
InterPro; IPR000023; Ppfruckinase.
Pfam; PF00365; PFK; 1.
PRINTS; PR00376; PFRCTKINASE.
PRINTS; PR00476; Ppfruckinase; 1.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
                                  Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlard D.J., Lee L.N., Lefkowitz E.J., Lu J., Matuushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Rochetson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                          "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=1256656; DOI=10.1073/pnas.0337704100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proton acceptor (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                 fructose 1,6-bisphosphate.
-!- PATHWAY: Key control step of glycolysis.
-!- SUBGELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphofructokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 1; Length 335; Pred. No. 6e+02;
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Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35213 MW; 930324A2307FFC6F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last amnotation update)
Transcription regulator of beta-galactosidase gene.
Name=lacR; OrderedLocusNames=lp_3470;
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(By similarity).
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            DOI=10.1128/JB.183.19.5709-5717.2001;
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ATP
ATP
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Deterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L., McDanald L.A., Feldblyum T.V., Angluoli S.V., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00476; PHFRCTKINASE.
Prodom; PD000707; PFFTUCKINASE; 1.
PROSITE; PS00433; PHOSPHOSPHOKINASE; 1.
Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                    Science 293:498-506(2001).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proton acceptor (By similarity)
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
                                                                                                                                                                                                                                                                                                                                                               fructose 1,6-bisphosphate.
--- PATHWAY: Key control seep of glycolysis.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
--- SIMILARITY: Belongs to the phosphofructokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%; Score 24; DB 1; Length 335; 71.4%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
6-phosphofructokinase (BC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-pfkA; OrderedLocusNames=spr0796;
Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2DFFBAACC58CAF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; F95103; F95103.
HSSP; P00512; 3PFK.
TIGR; SP0096; -
HAMAP; MF 00339; -; 1.
InterPro; IPR000023; Ppfruckinase.
Pfam; PF00365; PFK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21429245; PubMed=11544234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE007395; AAK75023:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35174 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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250
253
335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                 pneumoniae.";
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BINDING
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NP_BIND
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
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Best Local Similarity 71.4%;
Matches 5; Conservative 1
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                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 VMEVAEY 35
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                       01-OCT-2001 (
01-OCT-2001 (
01-MAR-2004 (
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                                                                                                                                                                                                                                              Clostridium
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Q7Q854;
                        Q97KM0
Q97KM0;
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A Atkina T. Crossman L.C., Pitt T., Churcher C., Mungall K.,
A Atkina T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
A Atkina T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bencley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
A Encley S.D., Sebaihia M., Crosset B., Davis P., Deshazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
A Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Songaiviai S., Stewns K., Tumapa S., Vesaratchavest M.,
Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
T. Perck Nath A. Nath A. March M. S. Mandileil",
Prock Nath A. Nath A. March M. S. Mandileil",
Prock Nath A. March M. S. Mandileil",
Prock Nath A. March M. March M. Mandileil",
Prock Nath A. March M. March M. Mandileil",
Prock Nath M. March M. March M. Mandileil",
Prock Nath M. March M. March
                                                                                                             "Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

EMBL; AL935262; CAD65557.1; -.

R RSSP; P15039; 1DBC.

R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003500; F:transcription factor activity; IEA.

R GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001981; HTH LacI.

R InterPro; IPR01982; Lambda_like_DNA.

R InterPro; IPR01982; Lambda_like_DNA.

R PROSTIE; PS:09032; Peripla_BP_1; 1.

R PROSTIE; PS:09032; HTH_LACI_2; 1.
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Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing
De Vos W.M., Siezen R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Burkholderiaceae, Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.8%; Score 24; DB 2; Length 336; Best Local Similarity 71.4%; Pred. No. 6.18+02; Matches 5; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 2; Length 337; 71.4%; Pred. No. 6.1e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL, BX571965; CAH35831.1; -.
SEQUENCE 337 AA; 34345 MW; 283FDDIDB18D947D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 AA; 37694 MW; 8DE5C36A11C2A419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Putative ribose transport system, permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 AA.
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=272560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K96243
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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RESULT 50

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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0004106; F:shikimate 5-dehydrogenase activity; IEA.
GO; GO:0010699; P:saromatic amino acid family biosynthesis, sh. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1128/JB.183.16.4838.2001,
Nocling J. Breton G. Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
J. Bacterium Clostridium accebobtylicum.";
J. Bacterium, ARV78873.4838(2001).
BENEL, ARV78675.
                                                                                                                                                         OrderedLocusNames=CAC0897;
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Pred. No. 6.6e+02;
1; Mismatches 1; Indels
                                                                           01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fusion: chorismate mutase and shikimate 5-dehydrogenase.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCPISCO2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA.
367 AA.
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Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR011342; AroE.
InterPro; IPR01242; AroE.
InterPro; IPR01279; CM mono_grmpos.
InterPro; IPR016151; Shikimate_DH.
Pfam; PF01817; CM 2; 1.
Ffam; PF0188; Shikimate_DH; 1.
TIGRFAMS; TIGR0567; aroE; 1.
TIGRFAMS; TIGR01805; CM mono_grmpos; 1
                                                      (TrEMBLrel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
EMBL; AAAB01008944; EAA10268.1;
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48 VMNMAEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabata S.
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                                                                                                                                                         Q9FNG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 54
                                                                                                              RESULT 53
                                                                                                                                       D9FNG6
                                                                                                                                                                                  à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Sarcu M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologia A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains I RING-type zinc finger.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                    ö
                                                                                                                                                                               82.8%; Score 24; DB 2; Length 375;
83.3%; Pred. No. 6.7e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.8%; Score 24; DB 2; Length 378; 71.4%; Pred. No. 6.8e+02;
GO; GO:0009966; P:regulation of signal transduction; IEA. GO; GO:0009607; P:response to bioric erimine. TEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L; BT000229; AANIS548.1; -. GO:000151; C:ubiquitin ligase complex; IEA. GO:000151; C:ubiquitin ligase complex; IEA. GO:0003676; F:ubiquitin-protein ligase activity; IEA. GO:0008270; F:zinc ion binding; IEA. GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00356; ZnF_C3H1, 1.
PROSITE; PS00518; ZF_RING 1; UNKNOWN_1.
PROSITE; PS50089; ZF_RING 2; 1.
Hypochetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 AA; 42518 MW; 142E4A6534BECA4D CRC64;
                                                                                                                                  375 AA; 43422 MW; B320E106818EC77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                   GO; GO:0009607; P:response to biotic stimulus; IEA InterPro; IPR007304; TAP42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein At5g06420.
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf_C3HC4; 1.
Pfam; PF00642; Zf_CCCH; 1.
                                                                                                                                                                                                                                    Conservative
                                                                                  Pfam; PF04177; TAP42; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SMART; SM00356; ZnF_C3F
                                                                                                                                                                                                                                                                                                                              291 MTVAEF 296
                                                                                                                                                                                                        Local Similarity
ses 5, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=At5g06420
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                                                                                                                                  SEQUENCE
                                                                                                                                                                                  Query Match
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081789
AC 081789
DT 01-0C
DT 01-0C
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DT 01-0C
DC SUKAT
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                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last annotation update)
Similarity to zinc finger protein (Hypothetical protein).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned PI clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
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EMBL; ABO06700; Eubiquitin ligase complex; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004842; F:nucleic acid binding; IEA.
GO; GO:0004842; F:zinc ion binding; IEA.
GO; GO:0016567; P:zinc ion binding; IEA.
InterPro; IPR000571; Znf_CCGH.
InterPro; IPR000871; Znf_CCGH.
Pfam; PF000697; Zf-CGCH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00186; ZnF C3H1; 1.
PROSITE; PS00618; ZF RING 1; UNKNOWN 1.
PROSITE; PS0069; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 AA; 42460 MW; 173D71BBBBBA3FE2D CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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   378 AA
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation.";
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Feldmann K.;
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Best Local Similarity 71.4 Matches 5; Conservative

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Gaps

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1; Indels

1; Mismatches

09730329-60ed.rup

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422 AA.
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    Helicobacteraceae; Wolinella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :|:|
285 VMAIADF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
                  NCBI_TaxID=844;
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Q8K164
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01-MAR.2004 (TrEMBLrel. 26, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
PREPROTEIN TRANSLOCASE SUBUNIT.
Wanne-SECY; OrderedLocusNames-WS1698;
Wolinella succinogenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                           Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Katayose Y.; "Oryas astiva nipponbare(GA3) genomic DNA, chromosome 6, clone:P0453H04."; GWA-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004776; BAD23066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 AA; 45695 MW; B125377DF01D82C3 CRC64;
                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 414 AA; 46194 MW; F7D292D41DF66FF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 2; I
57.1%; Pred. No. 7.4e+02;
iive 2; Mismatches 1;
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71.4%; Pred. No. 7.5e+02;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000182; GCN5acetyl trans.
Pfam; PF00583; Acetyltransf_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCN5-related N-acetyltransferase-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                  Hypothetical protein P0452F04.40
                                                                                                                                                                                                                                                                   InterPro; IPR008941; TPR-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 57.1
nes 4; Conservative
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200 VMTIADF 206
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es 5; Conserv
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                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=P0453H04.20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
                                          Name=P0452F04.40;
                                                                                                                                             NCBI_TaxID=39947;
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SEQUENCE 4
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25-OCT-2004
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Q7M8F1;
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1067UR2
AC Q67UR2
DT 25-0C
DT 25-0C
DT 25-0C
DE GCN5-
GN OCTYZE
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DOI=10.1128/JB.184.13.3614.3622.2002;
Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V.,
Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
"Genetic variation at the O-antigen biosynthetic locus in Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                           Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O., Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B., Meyer F., Lederer H., Schuster S.C., Francopiete genome sequence and analysis of Wolinella succinogenes."; Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
-!-FUNCTION: Involved in protein export (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the secx/SEC61-alpha family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00344; SecY; 1.
PRINTS; PR00303; SECYTRNLCASE.
TIGRRAMs; TIGR00967; 3a0501a007; 1.
PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
Complete protecome; Protein transport; Translocation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 82.8%; Score 24; DB 2; Length 419; Similarity 57.1%; Pred. No. 7.5e+02; 4; Conservative 2; Mismatches 1; Indels
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BEMBL, AF498401; AAM27508.1; ---

EMBL; AF499411; AAM27709.1; ---

GO, GO:000618; P:electron transport; IEA.

InterPro; IPR001732; UDPG MGDP dh.

Pfam; PF00984; UDPG MGDP dh.

Pfam; PF03720; UDPG MGDP dh. 1.

Pfam; PF03721; UDPG MGDP dh. 1.

Pfam; PF03721; UDPG MGDP dh. N; 1.

SEQUENCE 422 AA; 446019 MW; 28885984FB1A88A7 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Gaps

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RESULT 58

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de la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M., Heidelberg J.F., DeLong B.F.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUDMEd=14566056; DOI=10.1073/pnas.2133554100;
PubMed=14566056; DOI=10.1073/pnas.2133554100;
De La Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M., Heidelberg J., DeLong E.F.;
"Protecorhodopsin genes are distributed among divergent marine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Predicted metal-dependent amidase/aminoacylase/carboxypeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 426;
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                                                                                                                                                                                                                                                                                                                    Query Match 82.8%; Score 24; DB 2; Length 426
Best Local Similarity 71.4%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                            Carboxypeptidase.
SEQUENCE 426 AA; 46506 MW; 28B6CFFA7F07F438 CRC64;
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                                                                        Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databa EMBL, AY372453; AAR05239.1; -
GO, GO:0004109; F:carboxypeptidase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
InterPro; IPRO02933; Peptidase M20.
InterPro; IPRO10168; Peptidase M20.
Fam; PPO1546; Peptidase M20.
TIGRFAMS; TIGR01891; amidohydrolases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 100:12830-12835(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uncultured marine proteobacterium ANT8C10.
Bacteria; Proteobacteria; environmental samples.
NCBI_TaxID=248047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.8%; Score 24; DB 2; 171.4%; Pred. No. 7.6e+02;
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139 LMGVAEF 145
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Best Local Similarity
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[2]
SEQUENCE FROM N.A.
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SEQUENCE 426 A
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PubMed=14566056; DOI=10.1073/pnas.2133554100;

De La Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M., Heidelberg J., DeLong E.F.;

Herdelberg J., DeLong E.F.;

"Proteorhodopsin genes are distributed among divergent marine bacterial taxa.";

Proc. Natl. Acad. Sci. U.S.A. 100:12830-12835(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Predicted metal-dependent amidase/aminoacylase/carboxypeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AABF01000120; EAA23508.1; -.
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                                                                                                                                                                                                                                                                                                                      Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004352; F:glutamate dehydrogenase activity; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA. GO; GO:0006520; P:amino acid metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 AA; 46526 MW; 1269189AA6C03038 CRC64;
                                                                                                                                                                                                          ol-mak-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) NAD-specific glutamate dehydrogenase (EC 1.4.1.2). Name=FNV0417;
                                                                                                                                                                                                                                                                                                   Fusobacterium nucleatum subsp. vincentii ATCC 49256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uncultured marine proteobacterium ANT32C12.
Bacteria, Proteobacteria, environmental samples.
NCBI_TaxID=248048;
                                                                                                                                                             425 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
Pfam; PF00208; GLFV dehydrog_N.
Pfam; PF00208; GLFV dehydrog_N.
Pfam; PF002812; GLFV dehydrog_N.
PRINTS; PR00082; GLFDHDRGNASE.
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                                                       305 MAVAEF 310
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 49256;
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                  MXVAEF
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Best Loc Matches

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RESULT 59
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Pfam; PF03108; MuDR; 1.
SEQUENCE 442 AA; 50695 MW; 214F0711137BE6F1 CRC64;
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                                                                    Best Local Similarity
Matches 5, Conserv
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Q6ZS89
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Pubmed=12872003; DOI=10.1073/pnas.1533501100;
Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Facene Re Loned from Solanum bulbocastanum confers broad spectrum
resistance to potato late blight.";
Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133(2003).
Embl., ANJ 303171, AAP451871;
InterPro; IPR004312; MuDR.
InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.8%; Score 24; DB 2; Length 439; 71.4%; Pred. No. 7.8e+02; ive 1; Mismatches 1; Indels
                                                                                                                         Fuscoaccetium muclearum (subsp. muclearum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 AA; 48243 MW; AC999236B6713FD5 CRC64;
               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NAD-specific glutamate dehydrogenase (EC 1.4.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 AA.
                                                                                                           Fusobacterium nucleatum (subsp. nucleatum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative transposase-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=177013.38;
Solanum bulbocastanum (Wild potato)
                                                                                                                                                                                                                                              MEDLINE=21886394; PubMed=11889109;
                                                                                             OrderedLocusNames=FN0488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 VVAVAEF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 439 AA;
                                                                                                                                                                                                                              STRAIN=ATCC 25586;
                                                                                                                                                                  NCBI_TaxID=76856;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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SEQUENCE FROM N.A.

A Arita M., Musashin-Fujii A., Tanase T., Imose N., Takeuchi K.,
A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamamoto J., Isono Y.,
A Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
A Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
A Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
B Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
B CO: GO:0016502; E:ATPase activity, coupled to transmembrane m. ..; IEA.
GO: GO:001562; F:ATPase activity, coupled to transmembrane m. ..; IEA.
B RINTS; PRO0119; CATATPASE.
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                                                                               Gaps
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
NCBI_TaxID=5322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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h 82.8%; Score 24; DB 2; Length 442; Similarity 83.3%; Pred. No. 7.8e+02; 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 24; DB 2; Length 457; 71.4%; Pred. No. 8.1e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benito B.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ420741; CAD12640.1; -.
HSSP; P04191; 1SU4.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 AA; 51438 MW; E197444DDC2AF08A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ45732.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative ENA-ATPase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     457 AA
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84 VLLVAEF
                                                                                                                                                                                                                                                         DENTIFICATION
                                                                                                                                                                                Lewis S.E.;
                                                                                                                                                                                                             systematic
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SEQUENCE
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TRANSMEM
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Q9C7R2
      6,
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KRAIN-Berkeley;

KRAIN-Berkeley;

KRAIN-Berkeley;

KRAIN-Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Hederson S.N.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Hederson S.N.,

Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayaria A., An H.-J., Andrews-Prannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botharkov S.,

Borkova D., Botcham M.R., Buuck J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botharkov S.,

RA Beeson K.Y., Bullke C., Davemport L.B., Center A., Chandra I.,

Robon K., Doup L.E., Downes M., Digarle R., Center A., Chandra I.,

RA Goorn K.J., Evangelista C.C., Ferraz C., Ferriera S., Durkov B.C., Dunn P.,

RA Gober C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Hortin K.J., Evangelista C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P.,

RA Gober C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Houston K.A., Howlann T.J., Hernardez J.R., Houck J.,

Houston K.A., Howlann T.J., Mei M.-H., Ibegwan C.,

Jalali M., Kaluush F., Karpen G.H., Ke Z., Kamison J.A., Kalush F.,

RA Mount S.M., Mattei B., McIntoen T.C., McLeod M.P., McPherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,

Rainert K., Remington K.A., Howlann W., Strongs R., Sun E.,

Shrader B.C., Siden-Klamos I., Simpson M., Strongs R., Sun E.,

Shrader R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstenbach J.,

Walliams S.M., Woodey T., Wooley C., Morris C., Man G., Zhan M., Zhao Q., Zhan G., Zhan W., Zhuo S., Zhu X., Zhan S., Zhu X., Zhan S., Zhu X., Zhu 
                                                                                                                                                                                              ö
   . .; IEA.
                                                                                                                                                                                              Gaps
GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. GO; GO:0003824; F:Catalytic activity; IEA. GO; GO:0008812; P:Catalytic activity; IEA. GO; GO:000812; P:Cation transport; IEA. GO; GO:000812; P:Metabolism; IEA. From: PF007702; P:Metabolism; IEA. PRINTS; PR00119; CATATPASE. TIGREMAS; TIGR01494; ATPase_P-type; 1.
                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             82.8%; Score 24; DB 2; Length 463; 71.4%; Pred. No. 8.2e+02; tive 0; Mismatches 2; Indels
                                                                                                                                 49188 MW; C38AE05528AAFB28 CRC64;
                                                                                                                                                                                                                                                                                                                             G64F_DROME STANDARD; PRT; 469 AA. P83297; Q9VZJS; 28-F82003 (Rel. 41, Created) C5-UL-2004 (Rel. 44, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        Putative gustatory receptor 64f.
Name-Gr64f; ORFNames-CG32255;
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                             Local Similarity 71.4
                                                                                                                     463
                                                                                                                                                                                                                                                       347 VMTAAEF 353
                                                                                                                    463 AA;
                                                                                                                                                                                                                        1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                G64F_DROME
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                 RESULT 65
 84444444448
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                                                                                                                                     MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.B., de Grey A.D. M.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21407712; PubMed=11516643; DOI=10.1016/S0960-9822(01)00258-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunipace L., Meister S., McNealy C., Amrein H.;
"Spatially restricted expression of candidate taste receptors in the Drosophila gustatory system.";
curr. Biol. 11:822-835(2001).
-!- FUNCTION: Probable role in the gustatory response.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the G-protein coupled receptor Dr-tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003480; AAF47826.3; -.
FlyBase; EBGN0052255; Gr64f.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0008527; F:taste receptor activity; NAS.
GO; GO:0050909; P:perception of taste; NAS.
Fram: PF06151; Trehalose recp; 1.
G-protein coupled receptor; Hypothetical protein; Multigene family;
Bomain in the second of taste; NAS.
G-protein coupled receptor; Hypothetical protein; Multigene family;
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 469;
Pred. No. 8.3e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
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Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family. Subfamily II.
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146
167
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2220
2220
2265
3330
3351
3351
4435
435
                                                                                                                                                                                                                                                                                                                                                                                                              review.";
                                                                                                                   GENOME REANNOTATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H
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crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!-FUNCTION: Relaxes both positive and negative superturns and
-xhibits a strong decatenase activity. The B subunit binds ATP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: Heterotetramer of two subunits A and two subunits B (By
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MEDLINES, MEDLINES,
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Type II DNA topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B)
Name=top6B; OrderedLocusNames=APE0706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TOWN C.D., Kaul S.;
Submitted (GAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC068667; AAG51739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 484 AA; 52066 MW; F94D3EA5C96059B3 CRC64;
                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F15D2.29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 AA.
                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008892; WCOR413.
Pfam; PF05562; WCOR413; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 82.8%;
Local Similarity 71.4%;
nes 5; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E86416; E86416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeropyrum pernix.
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                                                                                                                                              Name=F15D2.29;
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09YE64;
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Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogtura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kadoh Y., Ramazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO1022; topeb; 1.
ATP-binding; Complete proteome; DNA-binding; Isomerase; Topoisomerase.
SEQUENCE 565 AA; 64096 MW; E4A3DFCC5E53D508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to the queuine tRNA-ribosyltransferase family.
EMBL; APD00005; BAA30215.1; -.
PIR; E71052; E71052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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PDB; 11T7; X-ray; A/B=1-582.
PDB; 11T8; X-ray; A/B=1-582.
PDB; 1J2B; X-ray; A/B=1-582.
GO; GO:0008479; F:queuine tRNA-ribosyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 1; Length 565; 83.3%; Pred. No. 9.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 AA.
                                                                                                                                                                     HSSP, O05207, 1MX0.
HAMAP; MF 00322; -; 1.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR0059734; DNA top5B.
InterPro; IPR010979; Ribosomal_H2TH.
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                                                                                                                                   EMBL; AP000060; BAA79682.1; -. PIR; B72660; B72660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein PH1116.
OrderedLocusNames=PH1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                  Pfam; PF02518; HATPase c; 1
SMART; SM00387; HATPase C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MXVAEF 7
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058843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 8.5e+02;
1; Mismatches 1; Indels
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InterPro; IPR004521; Unchar dom 2
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SEQUENCE
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MEDLINE-22511545; PubMed=12622808;

MEDLINE-22511545; PubMed=12622808;

Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,

A Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

An integrated analysis of the genome of the hyperthermophilic

Tachaeon Pyrococcus abyssis.";

Tachaeon Pyrococcus abyssis.";

Mol. Microbiol. 47:1495-1512(2003).

-I- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-

Geazagnanine in tRNAs with GU(N) anticodons (tRNA-Asp., -Asn.,-His

and -Tyr). After this exchange, a cyclopentendiol moiety is

attached to the 7-aminomethyl group of 7-deazaguanne, resulting

in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-
dihydraxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CORACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to the queuine tRNA-ribosyltransferase family.
EMBL; AJZ48266, CAB50027.1; -.
PIRE; AJZ48266, CAB50027.1; -.
PIR; F75090; F75090.
HSSP; O58843; 11Q8.
GO; GO:0008473; F:Queuine tRNA-ribosyltranbferase activity; IEA.
GO; GO:0008473; F:RNA binding; IEA.
GO; GO:000813; P:RNA binding; IEA.
GO; GO:0008033; P:RNA binding; IEA.
InterPro; IRR004804; ARNA_ribo_trans.
InterPro; IRR004804; ARNA_ribo_trans.
InterPro; IPR002616; tRNA_ribo_trans.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0008616; P:queucosine biosynthesis; IEA.
GO; GO:0008033; P:tRNA processing; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                        Complete protecome, Glycosyltransferase, Hypothetical protein,
Queuosine biosynthesis, Transferase, Zinc, tRNA processing.
SEQUENCE 582 AA, 66595 MW, B96F1D5EC0D73AC3 CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                               82.8%; Score 24; DB 2; Length 582; 57.1%; Pred. No. 1e+03; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Queuine-archaeosine tRNA ribosyltransferase.
                                                                                                                                                                                                                     SMART; SM0359; PUA; 1.
TIGRFAMS; TIGR00432; arcsn tRNA tgt; 1.
TIGRFAMS; TIGR00449; tgt_general; 1.
TIGRFAMS; TIGR00451; unchar_dom_2; 1.
                                                                                      InterPro; IPR004804; AtRNA_ribo_trans.
InterPro; IPR002478; PUA.
InterPro; IPR002616; tRNA_ribo_trans.
InterPro; IPR004521; Unchar_dom_2.
Pfam; PF01472; PUA; 1.
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Best Local Similarity 5...
4; Conservative
                                                                                                                                                                                                                                                                                                                     PROSITE; PS50890; PUA; 1
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440 VMAIAEY 446
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099UZNO
DD 0910ZNO
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GO; GO:0005534; C:nucleus; IEA.
GO; GO:00005534; F:ATP-binding; IEA.
GO; GO:0004003; F:ATP-bendent DNA helicase activity; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0001818; F:Mydrolase activity, acting on acid anhydrid. ..; I
GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. ..; I
GO; GO:0006289; P:nucleotide-excision repair; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE 21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P. Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Encephalitōzoon cuniculi GB-Mi.
Eukaryota, Fungi; Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=284813;
                                                                                                                                                                                                                              Complete proteome; Glycosyltransferase; Queuosine biosynthesis;
Transferase; Zinc; tRNA processing.
SEQUENCE 584 AA; 66667 MW; E31755EAE3681666 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                 Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP DEPENDENT DNA BINDING HELICASE (RAD3/XPD SUBFAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                          Query Match 82.8%; Score 24; DB 2; Best Local Similarity 57.1%; Pred. No. 1e+03; Matches 4; Conservative 2; ·Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICRFAMS; TIGRO0604; rad3; 1.
PROSITE; PS00690; DEAH ATP HELICASE; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            619 AA.
Pfam; PF01472; PUA; 1.
Pfam; PF01702; TGT; 1.
SMART; SM00359; PUA; 1.
TIGRPAM; TIGR00432; arcsn tRNA tgt; 1.
TIGRPAMs; TIGR00449; tgt general; 1.
TIGRPAMs; TIGR00445; tgt unchar dom 2; 1.
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InterPro; IPR002464; DEAH box.
InterPro; IPR006554; DENDG2.
InterPro; IPR006555; Helic c2.
InterPro; IPR001865; Ribosomal S2.
InterPro; IPR001945; XPD DNA_repair.
Pfam; PF0673; DEAD 2; 1.
SWART; SW00488; DEXDG2; 1.
SWART; SW00491; HELICC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                               PROSITE; PS50890; PUA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :||:
440 VMAIAEY 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ECU08 1120;
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NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=ileS;
                                       P91063
P91063;
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Q846V6
   RESULT 72
                       P91063
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STRAIN=ATCC 339313 NCPPB 528;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/4174599;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/4174599;

A sliva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A loagid R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alveb L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Ratelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locall E.C., Machado M.A., Madeira A.M.B.N., Martine F.G., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

A setubal J.C., Kitajima J.P.,

R. Comparison of the genomes of two Xanthomonas pathogens with differing the pereificities of two Xanthomo
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                         Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Score 24; DB 2; Length 619;
Pred. No. 1.1e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 AA; 76025 MW; C62FD2B62C18E793 CRC64;
                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417:459-463 (2002).

EMBL; AE012336; AAM41570.1; -..

EO, GO:00044871; F:signal transducer activity; IEA.

GO; GO:0001465; P:signal transduction; IEA.

InterPro; IPR002086; Aldehyd dehydrog.

InterPro; IPR011006; CheY like.

InterPro; IPR001633; EAL.

InterPro; IPR000160; GOBEF.
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Pfam; PF00990; GGDEF; 1.
SMART; SM00052, DUF2; 1.
IGRPAMS; TIGR00254; GGDEF; 1.
TIGRPAMS; TIGR00259; SENSORY, DOX; 1.
TIGRPAMS; TIGR0029; SENSORY, DOX; 1.
PROSITE; PS50687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
PROSITE; PS50887; GGDEF; 1.
                                                                                                                                                                                                             689 AA.
                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, C3
01-OCT-2002 (TrEMBLrel. 22, L6
01-OCT-2004 (TrEMBLrel. 26, L6
Hypothetical protein XCC2291.
 82.8%;
                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=XCC2291;
Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                               284 VMGVSEF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648 ILTVAÈF 654
                                                                            1 VMXVAEF 7
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Q8P8F1;
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Q8P8F1
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Yun H.J., Lee S.W., Yoon G.M., Kim S.Y., Choi S., Lee Y.S., Choi E.C.,
Kim S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                               Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                   WormBase Consortium; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.8%; Score 24; DB 2; Length 738; Best Local Similarity 83.3%; Pred. No. 1.3e+03; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; 108947; AAB37983.2; -.
PIR; 725551; 725551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans cosmid C17H11.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAND-Bristol N2;
Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; C17H11.2; Carrier
Hypothetical protein.
GroumNCE 738 AA; 83764 MW; D41414064A4944F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus
738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      871 AA
                                   01-MAY-1997 (TrEMBLrel. 03, Created) 01-OCT-2001 (TrEMBLrel. 18, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Hypothetical protein C17H11.2; Name=C17H11.2; Caenorhabditis elegans.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormBase, WBGene00015922; C17H11.2.
WormPep, C17H11.2; CE27703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q846V6;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soleucyl-tRNA synthetase.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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STRAIN=168;
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Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Vana Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-W.;

"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).

-!-CATALYTIC ACTIVITY: ATP L-isoleucine + tRNA(Ile) = AMP +

diphosphate + L-isoleucyl-tRNA(Ile).

-!-COFACTOR: Binds 1 zinc ion per subunit (By similarity).

-!-SUBUNIT: Monomer (By similarity).

-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!-SUMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 2; Length 871; 83.3%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100133 MW; 2E140C3F74318A15 CRC64;
                                                    GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                           Pfam; PF00133; ERNA-synt 1; 1.
PRINTS; PR00984; TRNASYNTHILE.
TIGRFAMS; TIGR00392; iles; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                             InterPro; IPR002300; tRNA-synt in.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002301; tRNA-synt ile.
InterPro; IPR009080; tRNAsyn is bind.
InterPro; IPR009080; Valks IIERS edit.
Pfan; PF00133; tRNA-synt i i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_lie.
InterPro; IPR009080; tRNAsyn_la_bind.
InterPro; IPR009008; ValRS_IleRS_edit
InterPro; IPR010663; ZF-FPG_IleRS.
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EMBL; AF516209; AAO65848.1; -. HSSP; P41972; 1FFY.
                                                                                                                                                                                                                                                                                                                                                                                                                       Aminoacyl-tRNA synthetase
SEQUENCE 871 AA; 10013:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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STRAIN=ATCC 12228;
PubMed=12950922;
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Q8CSX1;
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SYI_STAREP
DT 29-MA,
DD 129-MA,
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RA XARST R., Oggaswara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Bruschier L., Brans A., Braun O., Carter N.M.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entia C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Annes L.-M., Joris B., Kateger M., Liu H., Masuda S., Mauel C.,
Robayashi Y., Serliy M., Ogawa K., Ogiwara A., Oudega B.,
Rose M., Sadaie Y., Satol T., Scanlan E., Schleich S., Schroeter R.,
Rose M., Sadaie Y., Satol T., Scanlan E., Schleich S., Schroeter R.,
Annes M., Tamakoshi A., Tanaka T., Tarkagi T., Tarkagi T., Tarkamashi H.,
Rakmaru M., Vasata K., Vasati A., Wamane K., Wannier F.,
Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Andernegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Andernegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Andernegger T., Rinters P., Wipat A., Yamamoto H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Pfam; PF00133; tRNA-synt_1; 1.
Pfam; PF06127; zf-PPG IleRs; 1.
PRINTS; PR00984; TRNASYNTHIE.
PROSTURS; PR00984; TRNASYNTHIE.
PROSTUR; PS00178; AA_TRNA_LIGASE 1: 1.
PROSTUR; PS00178; AA_TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase; Mctal-binding; Protein biosynthesis; Zinc.
SITE 55 599 "MASKS: region.
SITE 55 599 "RNSKS: region.
BINDING 598 598 ATP (By similarity).
SEQUENCE 916 AA; 105185 MW; CS155509A91FCEEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYI_BACSU STANDARD; PRT; 921 AA.
045477; 031730; P71022;
041-071-0997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
1soleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 1; Length 916
83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ileS; OrderedLocusNames=BSU15430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%,
5; Conservative
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STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
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SECUENCE FROM N.A.

PubMed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,

Shores K.A., Foute D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,

Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pX01.";

Nucleic Acids Res. 32:977-988 (2004).

EMBL, AE017276, AAS42843.1; -.
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H., "Complete genome sequence of Bacillus cereus ZK."; submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         Score 24, DB 2; Length 921;
Pred. No. 1.6e+03;
0; Mismatches 1; Indels
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83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
                                                                                                                         EMBL; CP000001; AAU16613.1; -.
Aminoacyl-tRNA synthetase; Ligase.
SEQUENCE 921 AA; 104620 MW; PBF96E6AE4D5D3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104589 MW; B531AF210A8036C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Isoleucyl-tRNA synthetase (EC 6.1.1.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   921 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR001301; tRNA-synt_ile.
InterPro; IPR009000; tRNA-synt_la.
InterPro; IPR009000; valRS_I]eRS_edit.
InterPro; IPR010663; ZF-FPG_ILERS.
Pfam; PF00133; tRNA-synt_1; 1.
Pfam; PF00133; zf-PPG_ILERS; 1.
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PROSITE; PS00178; AA TRNA LIGASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=ileS; OrderedLocusNames=BCE3940;
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                                                                                                                                                                                                                                               82.8%;
                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 5; Conservative
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Q819R4
ID Q819R4
AC Q819R4
DT 01-JUN
DT 01-JUN
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R FIR; H69643; H6bc.

R HSSP; P41972; 10U3.

R HSSP; P41972; 10U3.

R HSSP; P41972; 10U3.

R Subtilist; BG11792; ileS.

R InterPro; IPR001300; tRNA-synt la.

R InterPro; IPR001300; tRNA-synt li.

DR InterPro; IPR009080; ValRS IleRS edit.

DR InterPro; IPR009080; ValRS IleRS edit.

DR InterPro; IPR009080; ValRS IleRS edit.

DR FAm; PF00133; ZF-PPG IleRS; 1.

DR PFMNTS; PR00984; TRNA-SYNT li. 1.

DR PROSITE; PS00178; AA TRNA LIGASE l; 1.

DR Aminoacyl-tRNA synthetase; ATP-binding; Complete protecome; Ligase;

KW Aminoacyl-tRNA synthetase; ATP-binding; Complete protecome; Ligase;

TTRR Synthetase; ATP-Binding; Complete protecome; Ligase;

KW Aminoacyl-tRNA synthetase; ATP-Binding; Complete protecome; Ligase;

TTRR Synthetase; ATP-Binding; Complete protecome; Ligase;

KW Aminoacyl-tRNA synthetase; ATP-Binding; Complete protecome; Ligase;

TTRR Synthetase; ATP-Bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                   Pragai Z., Tjalsma H., Bolhuis A., van Dijl J.M., Venema G., Bron S.; Submitted (FEB-1996) to the EMBL/Genbank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP + diphosphate + L-isoleucyl-tRNA(Ile).
-!- COFACTOR: Binds I zinc ion per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
1soleucine--tRNA ligase (Isoleucyl-tRNA synthetase) (EC 6.1.1.5).
Name=ileS; ORFNames=BTZK3654;
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83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=288681;
      Stewart G.C., Cha J.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                             SEQUENCE OF 733-921 FROM N.A.
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EMBL; U60901; AAB42280.1; -.
EMBL; U48870; AAB57764.1; -.
PIK; H69643; H69643.
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les 5; Conservative
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Q636D1
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STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.;
Fraser C.M.;
"Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AE017036; AAP27760.1; -.
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genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317; Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
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InterPro; IPR001310; tRNA-synt 1a.
InterPro; IPR001310; tRNA-synt 1a.
InterPro; IPR001301; tRNA-synt 1a.
InterPro; IPR009080; tRNAsyn 1a bind.
InterPro; IPR009080; tRNAsyn 1a bind.
InterPro; IPR009080; tRNAsyn 1a bind.
InterPro; IPR009081; tRNA-synt 1i. 1.
InterPro; IPR00131; tRNA-synt 1i. 1.
INTERPRAMS; TRGR00327; af-FPG 11eRS; 1.
ITGRRAMS; TRGR00327; af-FPG 11eRS; 1.
ITGR00327; af-FPG 11eRS; 1.
ITGRRAMS; TRGR00327; af-FPG 11eRS; 1.
ITGR00327; af-FPG 11eRS; af
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Pred. No. 1.6e+03;
0; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE117334; AAT33151.1; -. EMBL; AE017225; AAT56048.1; -. HSSP; P41972; 1FFY.
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                                    closely related bacteria.";
Nature 423:81-86(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoleucyl-tRNA synthetase.
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Best Local Similarity 83...
Local 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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TIGR; GBAA4034; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sterne;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Ames / isolate Porton;

MEDLINE=22608414; PubMed=12716.29; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Nelson K.E., Tettelin H., Fouts D.E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;
                                                                                                                                                                                                                                                                 MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Rapatral V., Bhattacharyya A., Reznik G., Mihailova N., Labidus A., Grechkin Y., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overboek R., Kyrpides N.C.; Overboek R., Kyrpides N.C.; Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
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R GO; GO:0004822; F:ATP binding; IEA.

R GO; GO:0004822; F:Isoleucine-tRNA ligase activity; IEA.

R GO; GO:000428; F:Isoleucine-tRNA ligase activity; IEA.

R GO; GO:000428; F:Isoleucyl-tRNA aminoacylation; IEA.

R InterPro; IPR001412; tRNA-synt_la.

InterPro; IPR001300; tRNA-synt_la.

InterPro; IPR001300; tRNA-synt_la.

InterPro; IPR009080; tRNA-synt_li.

R InterPro; IPR009080; tRNA-synt_li.

R InterPro; IPR009080; tRNA-synt_li.

R Pfam; PF06827; ZF-FPG IleRS.

R Pfam; PF06827; ZF-FPG IleRS; 1.

R Pfam; PF06827; ZF-FPG IleRS; 1.

R Pfam; PF06827; ZF-FPG IleRS; 1.

R PRINTS; PR00984; TRNASYNTHILE.

R PROSITE; PS00118; AA TRNA_LIGASE I; 1.

M Aminoacyl-tRNA synthetase; Complete proteome; Ligase.

SEQUENCE 921 AA; 104561 MW; 522D045A316EEIEO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 2; Length 921;
83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
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NCBI_TaxID=1392;
                                                                                           Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI TaxID=226900;
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O1-UIN-2003 (TrEMBLrel. 24, Created)
O1-UIN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Isoleucyl-tRNA synthetase
   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Isoleucyl-tRNA synthetase (EC 6.1.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 423:87-91(2003).
EMBL; AE017010; AAP10816.1; -.
                                                                         OrderedLocusNames=BC3895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 MTVAEF 120
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Matches
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081WE4
10 081WE
AC 081WE
DT 01-JU
DT 01-JU
DT 25-OC
GN Name=
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Q6G4C0
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"Complete genome sequence of Bacillus thuringiensis 97-27.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AR013355; AAT63892.1;
GO; GO:0005524; F:ATP binding, IEA.
GO; GO:0006528; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
150-JUL-2004 (TrEMBLrel. 27, Last annotation update)
150-JUL-2004 (TrEMBLrel. 27, Last annotation update)
180-JUL-2004 (TrEMBLrel. 27, Last annotation update)
180-JUL-2004 (TrEMBLrel. 27, Last sequence update)
180-JUL-2004 (Tr
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0
                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:00046428; P:isoleucine-tRNA ligase activity; IEA.
GO; GO:00046428; P:isoleucine-tRNA ligase activity; IEA.
GO; GO:00046428; P:isoleucine-tRNA aminoacylation; IEA.
InterPro; IPR001300; tRNA-synt_I.
InterPro; IPR001300; tRNA-synt_I.
InterPro; IPR001300; tRNA-synt_I.
InterPro; IPR001308; VANES IIERS edit.
InterPro; IPR00131; tRNA-synt_I.
InterPro; IPR00131; tRNA-synt_I.
InterPro; IPR00131; LRNA-synt_I.
InterPro; IPR00131; LRNA-SYNTHILE.
ITGRAMB; ITGR00132; ileS; I.
ITGR00132; ILES; I.
ITGR00132; AA TRNA_LIGASE I; I.
Aminoacy1-tRNA synthecase; Complete proteome.
SEQUENCE 921 AA; 104562 MW; 5D9A17ED5A741B9A CRC64;
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83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
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InterPro; IPR002300; ERNA-synt la.
InterPro; IPR002301; tRNA-synt li.
InterPro; IPR003080; tRNAsyn la bind.
InterPro; IPR009080; ValrS lleRS edit.
InterPro; IPR010663; ZF-FPG IIERS.
Pfam; PF00133; tRNA-synt l; l.
Pfam; PF06827; zf-FPG IIERS.
PRINTS; PR00984; TRNASYNTHIE.
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 MSVAEF 120
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SEQUENCE FROM N.A.

STRAIN-ATCC 49882 / Houston 1;

SINDER STRAIN-ATCC 49882 / Houston 1;

Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,

Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,

La Scola B., Holmberg M., Andersson S.G.E.;

"The louse-borne human pathogen Bartonella quintana is a genomic

derivative of the zoonotic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
EMBL; AE017333; AAU40657.1; -.
EMBL; CO000002; AAU23298.1; -.
Aminoacyl-ENA synthetase.
SRQUENCE 922 AA; 104355 MW; DFCB33B0F71906B6 CRC64;
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STRAINS-ATCC 14580;
STRAINS-ATCC 14580;
RESP M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J.
Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.
Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
Berka R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G., "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
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Pred. No. 1.6e+03;
0; Mismatches 1; Indels
                                                                                                                                              IleS (Isoleucyl-tRNA synthetase).
Name=ileS; ORFNames=BL02267, BLi01762;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                         25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
922 AA
                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
PRT;
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Best Local Similarity 83.3
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 MTVAEF 121
                                                                                                                                                                                                                                                                               NCBI_TaxID=279010;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DSM 13;
PubMed=15383718;
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Aminopeptidase; Glycoprotein; Hydrolase; Metalloprotease;
                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 86
AT9B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             086G73
                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  086G73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSEBBT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a microsomal aminopeptidase from the intestine of the nematode Haemonchus contortus."; blochim. Blophys. Acta 1338:295-306(1997).

-! CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|- Xbb- from a peptide, amide or arylamide. Xaa is preferably Ala, but may be most amino acids including pro (slow action). When a terminal hydrophobic residue is followed by a prolyl residue, the two may be released as an intact Xaa-Pro dipeptide.
-!- COPACTOR: Binds I zinc ion per subunit (By similarity).
-!- SINCELLULAR LOCATION: Type II membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Aminopeptidase N (EC 3.4.11.2) (Microsomal aminopeptidase) (Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97273974; PubMed=9128148; DOI=10.1016/S0167-4838(96)00204-X; Smith T.S., Graham M., Munn B.A., Newton S.E., Knox D.P., Coadwell W.J., McMichael-Phillips D., Smith H., Smith W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein H11).

Haemonchus contortus (Barber pole worm).

Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;

Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
R GO; GO:0000155; F:two-component sensor molecule activity; IEA.

GO; GO:000160; P:two-component signal transduction system (p. ..;
InterPro; IPR00163; EAL.

R InterPro; IPR00163; EAL.

R InterPro; IPR000160; GGDEF.

InterPro; IPR000014; PAS.

InterPro; IPR000014; PAS.

R Pfam; PP00563; EAL; 1.

R Pfam; PP00563; EAL; 1.

R SMART; SM00052; DUF2; 1.

R SMART; SM00052; DUF2; 1.

R TIGRPAMS; TIGR00225; GGDEF; 1.

R PROSITE; PS50883; EAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 24; DB 2; Length 961; 71.4%; Pred. No. 1.6e+03; rive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             971 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF01433; Peptidase M; 1.
PRINTS; PR00756; ALADIPTASE.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001930; Peptidase_M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X94187; CAA63897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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765 VMDLAEF 771
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AMPN HAREO
DY O107373
DY O1-NOV-
DY 25-ONT-
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ON NCBL TRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hidden antigen hll.
Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATOB HUMAN STANDARD; PRT; 1095 AA.
043861; 060872;
30-MAY-2000 (Rel. 39, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1) (HUSSY-
                 By similarity.
Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
Zinc (catalytic) (By similarity).
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
                                                                                                                                                                                               Proton donor (Potential).
N-linked (GlCNAc. ) (Potential).
N-linked (GlCNAc. ) (Potential).
N-linked (GlCNAc. ) (Potential).
N-linked (GlCNAc. ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY247714; AA091936.1; --
GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR001930; Peptidase_MI.
InterPro; IPR006025; Pept_M Zn_BS.
Pfam; PF01433; Peptidase_MI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                               Score 24; DB 1; Length 971;
Pred. No. 1.6e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.8%; Score 24; DB 2; Length 972; 71.4%; Pred. No. 1.6e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                        MW; 95C6A92B5CCA227C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Yan R.F., Li X.R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 972 AA; 110548 MW; 8DBC651B21D905D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20).
Name=ATP9B; Synonyms=ATPIIB, NEO1L;
    Transmembrane;
                                                                                                                                                                                                                                                                                                                                               Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00756; ALADIPTASE
                                                                                                                                                                                                                                                                                                               110542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                  971
378
379
382
401
465
98
226
548
857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 VISVAEF 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                              226
548
857
871 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VMXVAEF 7
Signal-anchor; TINIT MET 0 DOMAIN 1
                     0
                                                                                                       JOM.
METAL
TTE SITE
                                                                                                                                                                                                          ACT SITE CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                               SEQUENCE
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rissum=Brain;

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RA OLD T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibshara T., Tanaka T., Ishii S.,
Shiratori J. Saito K., Kawai Y., Isono Y., Nakamura Y.,
Nagahari K., Murakami K., Yawai Y., Isono Y., Nakamura Y.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Guna Y., Abe K., Kamihara K., Yakoi T., Puruya T., Kikkawa E.,
RA Jamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Tamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Ishida S., Ono Y., Takaguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Numara Y., Togiya S., Kommai F., Hara R., Takeuchi K., Atla M.,
RA Innose N., Mussahino K., Yuuki H., Oshima A., Saaski N., Aotsuka S.,
Momiyama H., Satoh N., Takami S., Terashima Y., Saroh S.,
Nomiyama H., Zatoh N., Takami S., Terashima Y., Saroh S.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Ramazaki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,
Ramadak K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikama Y., Okamoto S.,
RA Matsumura K., Nakajima Y., Milini Y., Takahashi Y., Nakagawa K.,
A Matsuhima -Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
A Matsuhima -Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
A Makai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Rawabata R., Nakajima Y., Milini Y., Olayano Y., Yamashita R.,
A Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Vamashita R.,
Rawalaki K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Rompali R., Nakai H., Nakamura N., Kikuchi H., Masuho Y., Vamashita R., Rompali R., Nakai R., Yada T., Nakamura N., Chulla R., Nakai R., Yada T., Nakaguto O., Isogai T., Saaki M., Ponomi R., Rompali R., Nakai R., Yada T., Nakaguto O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A SEQUENCE OF 208-1095 FROM N.A.

Birren B., Linton L., Nusbaum C., Lander E., Ali A., Allen N.,

Anderson S., Barna N., Bastien V., Boguslavkiy L., Boukhgalter B.,

Anderson S., Barna N., Bastien V., Boguslavkiy L., Boukhgalter B.,

A Choepel Y., Colangelo M., Collins S., Collymore A., Cook A.,

Cookel Y., Camarate J., Campopiano A., Chang J., Farreira P.,

A Bretlano K., Dawar K., Diaz J.S., Dodge S., Faro S., Ferreira P.,

A Bratalano K., Dawar K., Diaz J.S., Dodge S., Faro S., Ferreira P.,

A Bratasa A., Kells C., Lander B., Heaford A.,

A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,

A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,

A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,

A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,

A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,

A Horton L., Hulme W., Iliev I., Johnson R., McKernan K.,

A Marquis N., Matthews C., McCarthy M., McEwan P., McKernan K.,

A Maylor J., Nguyen C., Norbu C., Norman C.H., O'Connor T.,

A Popheeters R., Meddrim U., Rosetti M., Roy A., Santos R.,

A Pierre N., Pollara V., Raymond C., Retta R., Rieback M., Riley R.,

A Schauer S., Schupback R., Seaman S., Severy P., Spencer B.,

Stange-Thomann N., Stojanovic N., Strauss N., Subramanian A.,

A Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Travis N.,

A Talamas J., Yesialiev H., Viel R., Vo A., Wilson B., Wu X., Wyman D.,

Ne W.J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel R.A.; "Multiple members of a third subfamily of P-type ATPases identified by genomic sequences and ESTs."; Genome Res. 8:354-361(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                  PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98217376; PubMed=9548971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE OF 759-1095 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
SEQUENCE OF 768-1095 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet. 36:40-45(2004).
                                                                           SEQUENCE OF 1-420 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
DOO COC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:13541; ATTORNEY: AGENCY GENEW; HGNC:13541; ATTORNEY: AGENCY HGNC:13541; ATTORNEY: AGENCY HGNC:13541; ATTORNEY: AGENCY GO: GO:0016221; C:integral to membrane; NAS.

GO; GO:0015247; F:aminophospholipid transporter activity; NAS.

GO; GO:001529; F:cation-transporting ATPase activity; NAS.

GO; GO:0015917; P:aminophospholipid transport; NAS.

GO: GO:0015917; P:aminophospholipid transport; NAS.

InterPro; IPR001537; ATPASE E1-E2.

InterPro; IPR008334; Dehal Iike hydro.

R InterPro; IPR008339; Rilpase.

R InterPro; IPR00839; Rilpase.

R Pfam; PF00122; B1-E2 ATPASE.

R Pfam; PF00122; GATAPPASE.

R Pfam; PF00152; CATAPPASE.

R TIGRNIS; PR00119; CATAPPASE E1-E2, 1.

R PROSITE; PS00154; ATPASE E1-E2, 1.

M ATP-binding; Hydrolase; Magnesium; Multigene family; Phosphorylation;
                                                                                                                                                                                                                          Unpublished observations (JUL-2002).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
MEDLINE=21064499; PubMed=11124703; DOJ=10.1002/1097-0061(200101)18:1x69::AID-YEA647>3.3.CO;2-8; DOJ=10.1002/1097-0061(200101)18:1x69::AID-YEA647>3.3.CO;2-8; Stanchi F., Simionati B., Cannata N., Zimbello R., Lanfranchi G., Valle G.; Cannata N., Zimbello R., Lanfranchi G., Valle G.; Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-aspartylphosphate intermediate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Potential.
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Extracellular (Potential)
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Potential.
Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular (Potential)
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D -> N (in Ref. 3)
R -> K (in Ref. 3)
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EMBL, AC104423; -; NOT ANNOTATED CDS.
EMBL, U78978; AAC05243.1; -.
EMBL, AJ006268; CAA06934.1; -.
                                                                                                                                                                                     CONCEPTUAL TRANSLATION.
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                                                                                                                    yeast sequences."
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non-profit institutions as long
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InterPro; IPR001757; AtPase B1-E2.
InterPro; IPR005834; Dehal Ike hydro.
InterPro; IPR006539; B1-E2 ArPase_reg.
InterPro; IPR006539; F1ippase.
Fini; PF000122; B1-E2 ArPase; I.
Pfam; PF00702; Hydrolase; I.
PRINTS; PR00119; CATATPASE.
TIGRPAMS; TIGR01652; ATPASE_P1ipid; I.
PROSITE; PS00154; ATPASE_E1_E2; I.
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NCBI_TaxID=6239;
                                           entities requires a license agreement ( or send an email to license@isb-sib.ch)
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1095 AA; 123546
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71.4%;
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Query Local Similarity 71.4%,
Best Local Similarity 71.4%,
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VAB1_CAEEL
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Altilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevichenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rochnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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-! CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

-! SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUB SPECIFICITY: Found in most tissues except spleen and muscle. Most abundant in testis. Also detected in fetal tissues.

-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases).
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ICR; TISSUE=Brain; MEDLINE=22473714; PubMed=11015572; Halleck M.S., Lawler U.F. Jr., Blackshaw S., Gao L., Nagarajan P., Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D., Williamson P., Schlegel R. N.; "Differential expression of putative transbilayer amphipath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                          ATOB MOUSE STANDARD; PRT; 1095 AA.
P98195; Q99L13;
30-MAY-2000 (Rel. 39, Created)
28-FEB--2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1).
                                                                                                                                                                   Length 1095;
S -> I (in Ref. 3).
E -> D (in Ref. 3).
E -> D (in Ref. 3).
R -> K (in Ref. 3).
D -> N (in Ref. 3).
K -> N (in Ref. 3).
K -> N (in Ref. 3).
S -> N (in Ref. 3).
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Pred. No. 1.8e+03;
                                                                                                                                                                                                          1; Mismatches
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AT9B_MOUSE
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10-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Bphrin receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein kinase
Eph receptor) (Variable abnormal protein 1).
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Pred. No. 1.8e+03;
1; Mismatches 1; Indels
as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; A0176FEASDFEA179 CRC64;
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                           modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available,
TISSUE SPECIFICITY: During ventral enclosure of the epidermis,
expression is seen in clusters of presumptive head neuronal cells
and several cells in the tail region. Early larvae show expression
in the nerve ring and ventral nerve cord. Strong expression is
also seen in the procorpus and terminal bulb of the pharynx.
Expression in the nervous system is seen through to adulthood.
SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
sceptor subfamily.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                   Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for members of the ephrin family. Involved in interactions between neuronal substrate cells and a migrating epithelial sheet in head epidermis morphogenesis. Also required for cell movements following gastrulation and during ventral
             MEDLINE=98165343; PubMed=9506518; DOI=10.1016/S0092-8674(00)81131-9; George S.E., Simokat K., Hardin J., Chisholm A.D.; "The VAB-1 Eph receptor tyrosine kinse functions in neural and epithelial morphogenesis in C. elegans.";
                                                                                                                                                                                                                                                                                                                                                  closure of the epidermis.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                         The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wormmep; Manage (1986)

Wormmep; Mo3A1.1b; GE2660.

Wormmep; Mo3A1.1b; GE2660.

Wormmep; Mo3A1.1b; GE2660.

GO; GO: 0016021; C: integral to membrane; ISS.

GO; GO: 0005003; F: ephrin receptor activity; ISS.

GO; GO: 0007331; F: protein-tyrosine kinase activity; ISS.

InterPro; IPR001090; Ephrin receptor.

InterPro; IPR001995; FW III-1ike.

InterPro; IPR001995; FW III-1ike.

InterPro; IPR00179; Prot kinase.

InterPro; IPR00179; Prot kinase.

InterPro; IPR00179; Tyr pkinase.

InterPro; IPR00145; Tyr pkinase.

InterPro; IPR0044; Ephrin lbd; 1.

Pfam; PF01404; Ephrin lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=061460-2; Sequence=VSP_050207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=O61460-1; Sequence=Displayed;
                                                                                                                                                                                                                                       REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormBase; WBGene00006868; vab-1.
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                                                                             Cell 92:633-643(1998)
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Waterston R.;
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T->1: In allele e699; most die as larvae.
E-XK: In allele e856; most die as larvae.
G-SE: In allele e2; most die as adults.
C->F: In allele ju22; most die as adults.
C->Y: In allele e1063; most die as
                                                   SMART; SMO0601; FN3. 2.
SMART; SM00601; FN3. 2.
SMART; SM0019; TyrKc; 1.
PROSITE; PSO0107; PROTEIN KINASE ATP; 1.
PROSITE; PSO0109; PROTEIN KINASE DOM; 1.
PROSITE; PSO0109; PROTEIN KINASE TYR; FALSE NEG.
Alternative splicing; ATP-binding; Developmental protein;
Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transferase;
Transmembrane; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-11nked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential).
Missing (in 160form b).
FrId=VSP 050007.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotyrosine (by autocatalysis) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphotyrosine (by autocatalysis) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphotyrosine (by autocatalysis) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphotyrosine (by autocatalysis)
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0
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                                                                                                                                                                                                                                                                                                                                                            Protein kinase.
PDZ-binding motif (Potential).
ATP (By similarity).
ATP (By similarity).
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW; 6E4A3037BB92A1D0 CRC64;
                                                                                                                                                                                                                                              Ephrin receptor 1.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. .) (F
                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                              Cys-rich.
Fibronectin type-III 1.
Fibronectin type-III 2.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y75B7AL.4.
Name-Y75B7AL.4; ORFNames=Y75B7AL.4;
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity
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                                                                                                                                                                                                                               Potential
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          PRINTS; PR00109; TYRKINASE.
ProDom; PD001495; Ephrin receptor; 1.
ProDom; PD000001; Prot_kinase; 1.
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71.4%;
Pfam; PF00069; Pkinase; 1.
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1122
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436
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Best Local Similarity
Matches 5; Conserv
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TRANSMEM
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MOD_RES
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1096558
AC 096558
DT 01-MM
DT 01-MM
DT Name-I
GN Name-I
GN Caeno
OC Bukary
OC Rukary
OC NCBI
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and mouse
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                           Q68FM3
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Matches
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                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEGUENCE 1130 AA; 123777 MW; FACO55A8A919C8E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024869; AAK68606.2; -.
                                                                                                            "The sequence of C. elegans cosmid Y75B7AL."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               STRAIN-Bristol N2, Waterston R.H.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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WormPep; Y75B7AL.4; CE32278.
InterPro; IPR000199; RhoGAP.
InterPro; IPR009316; RhoGAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
                  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                    Waterston R.;
Submitted (MAY-2002)
                                                                                                                                                                                                                                                                                                                                                  warerston K.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Submitted (NOV-2002)
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Submitted (JAN-2003)
                                                                                                                                                                                                                Submitted (JUN-2001)
                                     WormBase Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Bristol N2,
Waterston R.;
                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
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STRAIN=Bristol N2;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSIB=Brain;

Rubbed=1247932; DOI=10.1073/pnas.242603899;

Rubbed=12477932; DOI=10.1073/pnas.242603899;

Rausener R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

Altschul, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

A plachul R.F., Jordan H., Moore T., Max S.I., Mang J., Haide F.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raheeley R.W., Touchman J.W., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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TIGREAMS; TIGRO1494; ATPASS P-type; 4.
PROSITE; PSO154; ATPASE BIE2; UNKNOWN 1.
SEQUENCE 1146 AA; 129044 WW; FF07AFD694A1830E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (MUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079626; AAH79626.1; -.
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Last annotation update)
                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 1.9e+03;
1; Mismatches 1;
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PRT; 1146 AA
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InterPro; IPR005834; Dahal like hydro.
InterPro; IPR005139; Plippase.
Pfam; PF00702; Hydrolase; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%;
                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4 es 5; Conservative
PRELIMINARY;
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1067 LMVVAEF 1073
                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VMXVAEF 7
                                                                                                                                                          Atp9b protein.
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542

537 MSVAEF

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2 MXVAEF 7

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2201 AA.
                                                                                                                                                                                                                            PRT; 2033 AA
  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27,
  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces thioluteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: ||||
1843 ILAVAEF 1849
                                                                                                  1173 VLDVÁĚÝ 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1KEZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                   1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=aurC;
                                                                                                                                                                                                                          07XI95
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     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 94
                                                                                                                                                                             RESULT 93
                                                                                                                                                                                                       Q7XI95
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MEDLINE=2297040; PubNed=14621292;
MARAIN-PCC 7421;
MARAINEZ277040; PubNed=14621292;
MARAINEZ277040; PubNed=14621292;
MARAINEZ277040; MARAINE R., Mishida Y., Kiyokawa C.,
Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of Gloeobacter violaceus PCC 7421, a
"Complete genome structure of Gloeobacter violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
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"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
"Complete genome structure of Gloeobacter Violaceus PCC 7421, a
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  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                MEDLINE=22531580; PubMed=12644555; DOI=10.1093/molbev/msg031;
Kojima K.K., Fujiwara H.;
"Evolution of target specificity in R1 clade non-LTR
                                                                                                                                                                                          MO1. Biol. Evol. 20:351-361(2003).

EMBL; AB090822; BAC57920.1; -.

GO; GO:000323; F:RNA binding; IEA.

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:006578; P:RNA-dependent DNA replication; IEA.

InterPro; IPR005135; Exo_endo_phos.

InterPro; IPR0009477; RVTse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 2; Length 1566; Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.8%; Score 24; DB 2; Length 1173; 83.3%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF031372; Exo endo phos; 1.
Pfam; PF00178; RVT 1; 2.
PROSITE; PS00904; PPTA; UNKNOWN 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1173 AA; 132166 MW; AF60298E9A9D67B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, Q55418; 1MM8.

GO; GO:0004519; F:endonuclease activity; IEA.

GO; GO:0016539; F:inteln-mediated protein splicing; IEA.

InterPro; IPR006142; INTEIN.

InterPro; IPR004042; Inteln_endonuc.

InterPro; IPR006141; Inteln_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeobacter violaceus.
Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
NCBI_TaxID=33072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0379; INTEIN.

TIGREAMS; TIGRO1443; intein Cterm; 2.

TIGREAMS; TIGRO1445; intein Cterm; 1.

PROSITE; PS50818; INTEIN C TER; 2.

PROSITE; PS50819; INTEIN ENDONUCLEASE; 2.

PROSITE; PS50817; INTEIN TER; 2.

Complete proteome.

SEQUENCE 1566 AA; 172226 MW; 907814D1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=gll3966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 MTVAEF 99
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Best Local Similarity
                                                                                                                                                                           retrotransposons."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gll3966 protein.
                         NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 92
Q7NEB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
셤
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Gaps
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PubMed=14700630; DOI=10.1016/j.chembiol.2003.11.009;
PubMed=14700630;
Literation as programmed event during polyketide assembly; molecular analysis of the aurecthin biosynthesis gene cluster.";
Chem. Biol. 10:1225-1232(2003).
EMBL; AJ575648; CAE02606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                    O7X195;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein P0453G03.24.
Name-p0453G03.24;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0048037; F:cofactor binding; IEA.
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
InterPro; IPR001227; Ac_transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=66431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 2; Length 2033;
Pred. No. 3.38+03;
2; Mismatches 1; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; Q7X195; -.
InterPro; IPR000413; Integrin alpha.
PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 2033 AA; 221848 MW; 247BFD68BD43562C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:P0453G03.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004276; BAC79823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Polyketide synthase type I.
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G62 protein (E7 protein) (Fragment)
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E59 protein (Fragment).
                                                                                                                                                   Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Matches
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 2; Length 2201; Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJOO02918; CAAO Pinding, IEA.
GO; GO:0004713; F.ATP binding, IEA.
GO; GO:0004713; F.PATP binding, IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
THEATPHO: IPRO00719; PROCE kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 2; Length 53;
Pred. No. 2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233522 MW; 11440F4B7192A336 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q712V2;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein tyrosine kinase (EC 2.7.1.112) (Fragment).
Name=DmHD-311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                PROSITE; PS50075; ACP DOMAIN, 2.
PROSITE; PS00006.B KETOACYL, SYNTHASE; 2.
PROSITE; PS00120; LIPASE SER; UNKNOWN 1.
PROSITE; PS00121; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Prot Kinase; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. Kinase; Transferase.
                                 InterPro; IPR008262; Lipase_AS.
InterPro; IPR006163; Phsppanteth_bind.
                                                                                      InterPro; IPR006162; Ppantne S. —
InterPro; IPR001031; Thioesterase.
Pfam; PF00698; Acyl transf 1; 2.
Pfam; PF00109; Ketoacyl-synt; 2.
Pfam; PF02801; Ketoacyl-synt; 2.
Pfam; PF00550; PP-binding; 2.
Pfam; PF00975; Thioesterase: 1.
   InterPro; IPR000794; Ketoacyl_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphopantetheine, Transferase.
SEQUENCE 2201 AA; 233522 MW;
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Matches 4; Conservative
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Matches 5; Conservative
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VMKIADF 14
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Q91995
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Brandli A.W., Kirschner M.W.;
"Molecular cloning of tyrosine kinases in the early Xenopus embryo:
identification of Eck-related genes expressed in cranial neural crest
cells of the second (hyoid) arch.";
Dev. Dyn. 203:119-140(1995).
EMBL; U11730; AAA91293.1; -.
HSSP; P11362; 2FGI.
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Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
Probom; PD000011; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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EMBL; U1173; AAA91286.1; -.

EO, GO:0005524; F:ATP binding; IEA.

GO; GO:0004672; F:protein kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.

InterPro; IPR000719; Prot_Kinase.

ProDom; PD000011; Prot_Kinase;

PROSITE; FS50011; PROTEIN_KINASE_DOM; 1.
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Pred. No. 2.1e+02;
2; Mismatches 1; Indels
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Pred. No. 2.1e+02;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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MEDLINE-95383727; PubMed=7655077;
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MEDLINE=95383727; PubMed=7655077;
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Receptor.
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Q9P166
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MEDLINE=93096484; PubMed=1281307;

A chestier A., wilkinson D.G., Charnay P.;

Thatdi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.G.,

Giladdi-Hebenstreit P., Sieto M.A., Frain M., Mattei M.G.,

That Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";

Loncogene 7.1499-2506(1992).

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006472; F:protein kinase activity; IEA.

R GO; GO:0006468; P:protein mino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.

InterPro; IPR00019; Frot kinase.

R Probom; PD000001; Prot kinase; 1.

R PROBOM; PROFEIN KINASE DOM; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-NOV-1996 (TrEMBLrel. 101, Last sequence update)
01-NOT-1996 (TrEMBLrel. 25, Last annotation update)
Coturnix coturnix fibroblast growth factor receptor, clone H7
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GO; GO:0004672; F:protein kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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     Indels
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Last annotation update)
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2; Mismatches
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Oncogene 7:2479-2487(1992).
EMBL; XG963; CAA49363.1; -.
HSSP; P11362; 2FGI.
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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4; Conservative
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11 VMKIADF 17
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VMKIADF 18
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Best Local Similarity
Matches 4; Conserv
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Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2.38+02;
2; Mismatches 1; Indels
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Pred. No. 2.2e+02;
2; Mismatches 1; Indels
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57 57
57 AA; 6523 MW; 8DAA6A71E3F1B45E CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Proc Kinase.
Probon; PD00001; Prot Kinase; 1.
PROSITE; PS50011; PROTĒIN_KINASE_DOM; 1.
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Job time : 123 secs
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Similarity 57.1%;
4; Conservative 2
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4; Conservative
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12 VMKIADF 18
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27 ILKVAEF 33
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Best Local Similarity
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Streptoco
Soybean p
DegP prot
 Angiogene
Bacterial
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This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or associated with the synthesis, metabolism or degradation of carbobydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is the sequence of a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO at tpp.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; ds; plant.
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AD141765
AD221260
ADS2320
AD808788
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ADR31649
ADR14553
AAY70554
                           ADB65129
ABM81168
                                                                       ADF05584
AAY97667
ABU30670
ABB93670
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ABB79513
ABJ19407
ADAS4722
ABU08528
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AAG51020
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                                                                                                                                                                                                                                                                                   18-DEC-2003
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plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;

RESULT 1 4DC07972

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Candida tropicalis transformation system - using host auxotrophic in an amino acid, purine or pyrimidine pathway as result of mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                         The gene product (and opt. the URA3 B gene product - AAR06640) is used to complement an auxotrophic host to prototrophy. The host may be defective in orotidine-5'-phosphate decarboxylase activity. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome P450 nicotine adenine dinucleotide phosphate oxidoreductase and cytochrome P450 monooxygenase nucleic acids and encoded proteins, useful for overproducing dicarboxylic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URA3; URA integration vector; cytochrome P450; NADPH reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score.19; DB 2; I
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eirich LD, Eshoo M,
loper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                           Cregg JM, Gleeson MA, Picataggio S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY90608 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida tropicalis URA3A protein.
                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loper JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida tropicalis; ATCC20366
                                     89US-00308481
                                                                            89US-00308481
89US-00386837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0103099P.
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monooxygenase; CYP52A; CPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                      RES CORP
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Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                  WPI; 1990-275138/36.
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                                                                                                                                                                                                                                       N-PSDB; AAQ05864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ05864-Q05866
                                                                                                                                      (HENK ) HENKEL
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                                     08-FEB-1989;
                                                                          08-FEB-1989;
                                                                                                 27-JUL-1989;
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10-MAR-1999;
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23-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY90608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mNNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as artibodiss, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the ODNA molecules. As such, these concludes are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for concluded to a morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, noctropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence of the invention but sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                          New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                          Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uracil biosynthetic pathway; orotidine-5'-phosphate decarboxylase;
URA3 A gene; auxotrophe; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orotidine-5'-phosphate decarboxylase encoded by the URA3 A gene.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 8; Length 243;
Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3967; 2686pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR06639 standard; protein; 267 AA.
                                                                                                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                         14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
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                                                                                                                                    12-FEB-2004; 2004EP-00003145.
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Best Local Similarity 57.1
A; Conservative
                                                                                                                                                                                                                                                                        Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 VATAAEF 207
                                                                                                                                                                                                                                                                                                                                    WPI; 2004-583265/57
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                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADR10422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 243 AA;
                                                                                                                                                                     14-FEB-2003;
                  Homo sapiens
                                                       EP1447413-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-1991
                                                                                             18-AUG-2004.
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Gaps

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3; Indels

Length 267;

Cornett CA;

Madduri KM,

Example 15; Fig 23; 200pp; English

WO9009449-A.

AAR06639;

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98US-0103099P.

05-OCT-1998; 10-MAR-1999;

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The invention relates to 12 novel genomic DNA sequences and proteins which are components of the omega hydroxylase complex of Candida tropicalis ATCC 20366. The DNA sequences (AAA3066-A3057) respectively encode cytochrome P450 NADPH oxidoreductases CPRA and CPRB (AAY90596, AAY90595) and cytochrome P450 monoxygenases CPRSAAAA, CYPSAABA, CYPSAABA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 19; DB 3; Length 267; 57.1%; Pred. No. 1.8e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU12099 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida tropicalis URA3A protein.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida tropicalis; 20336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 267 AA;
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23-APR-2002
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99US-00302620 98US-0083798P

30-APR-1999; 01-MAY-1998;

US6331420-B1

18-DEC-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding cytochrome P450 and NADPH reductase enzymes of omega-hydroxylase complex of Candida tropicalis, useful for increasing production of dicarboxylic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; enzyme; yeast; omega oxygenase complex; cytochrome P450 monooxygenase; CYP; NADBH reductase enzymes; CPR; CPRA; CYPS2A1A; CYPS2A2A; CYPS2A3A; CYPS2A3B; CYPS2A5B; CYPS2A5A; CYPS2A5B; CYPS2ASB; CYPSZASB; CYPSZASB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eirich LD, Eshoo M, oper JC, Gleeson M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; Fig 23; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loper JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-138383/18
                                                                                                                                        CRAFT D L.
EIRICH L D.
                                                                                               WILSON C R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003049821-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK31897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC44987;
                                                                                                                                                                                                                                                                                                                                                                                               (LOPE/)
(GLEE/)
                                                                                                      (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                         (CORN/)
(BREN/)
                                                                                                                                                                                                                                                                                                                                                                 TANG/)
                                                                                                                                                                                                                 ESHO/)
                                                                                                                                                                                                                                                          MADD/)
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8
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The invention relates to an isolated nucleic acid selected encoding Candida tropicalis omega oxygenase complex enzymes (CPR) designanced P450 monooxygenase (CPP) and NADPH reductase enzymes (CPR) designated CPRA, CPPS2A1A, CYPS2A2A, CYPS2A3A, CYPS2A3B, CYPS2A3B, CYPS2A3A, CYPS2A3B, CYPS2A3B, CYPS2A3B, CYPS2A3B, CYPS2A3A, CYPS2A3B, CYPSAB4, CYPS2A3B, CYPS2A3B, CYPS2AB, CYPSZAAB, CYPSZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene; enzyme; yeast; omega oxygenase complex; cytochrome P450 monooxygenase; CYP; NADPH reductase enzymes; CPR; CPRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids that may be utilized as industrial intermediates in manufacturing
                                                                                                                                                                                                                                                                                                                                                                                        Madduri KM, Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 19; DB 7; Length 267
57.1%; Pred. No. 1.8e+03;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        , Eshoo M,
Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; SEQ ID NO 106; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC45557 standard; protein; 267 AA
                                                                                                                                                                                                                                                                                                                                                                                        Birich LD,
                                                                                                                                                                                                                                                                                                                                                                                                               Loper JC,
                 98US-0083798P.
98US-0103099P.
99US-0123555P.
99US-00302620.
                                                                                                         2001US-00976800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 57.1
Les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diesters and polymers.
                                                                                                                                                                     CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast URA3A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-777150/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 VTTTAEF 45
                                                                                                                                                   WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                   TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADC44986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 267 AA;
                                          05-OCT-1998;
10-MAR-1999;
                                                                                                           12-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                               Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2003
                                                                                       30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                        Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC45557;
                                                                                                                                                                                                                                                                               (BREN/)
(TANG/)
                                                                                                                                                                                                                                                                                                                         (LOPE/)
(GLEE/)
                                                                                                                                                   (MILS/)
                                                                                                                                                                                                                                                           (CORN/)
                                                                                                                                                                                              (EIRI/)
                                                                                                                                                                                                                  (ESHO/)
                                                                                                                                                                                                                                      (MADD/)
                                                                                                                                                                          (CRAF/)
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Matches
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The invention relates to an isolated nucleic acid selected encoding Candida tropicalis omega oxygenase complex enzymes (cytochrome P450 monooxygenase (CYP) and NADPH reductase enzymes (Cytochrome P450 conocytenase (CYP) and NADPH reductase enzymes (CPPSAAB, CYP52AB, CYP5AB, CYP5AB,
             CYP52A5B; CYP52A8A; CYP52A8B; CYP52D4A; dicarboxylic acid; diester; polymer; thermoplastic; plasticising agent; lubricant; hydraulic fluid; agricultural chemical; pharmaceutical; dye; surfactant; adhesive; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids that may be utilized as industrial intermediates in manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madduri KM, Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eirich LD, Eshoo M,
Loper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; SEQ ID NO 106; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loper JC,
                                                                                                                                                                                                                                                                                 98US-0083798P.
98US-0103099P.
99US-0123555P.
99US-00302620.
                                                                                                                                                                                                                                          03-MAY-2002; 2002US-00139031.
                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001; 2001US-00976800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diesters and polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craft DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                    CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-765370/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                            Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADC45556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 267 AA;
                                                                                                                                                     US2003049822-A1
                                                                                                                                                                                                                                                                                      01-MAY-1998;
                                                                                                                                                                                                                                                                                                          35-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brenner AA,
                                                                                                                                                                                                                                                                                                                             10-MAR-1999
                                                                                                                                                                                                 13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                    (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TANG/)
(LOPE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORN/)
(BREN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MADD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cytochrome P450 and NADPH oxidoreductase, i.e. CPR and CYP, genes and proteins, useful for discriminating members of a gene family by quantifying the amount of target mRNA in a sample, or for omega-oxidation of long chain fatty acids.
                                                                                                                                                             Yeast, enzyme; cytochrome P450; CYP; NADPH reductase; CPR; omega-hydroxylase complex; omega-oxidation; long chain fatty acid; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Madduri KM,
                                                                                                                              Integration vector pURA2in URA3A gene encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Eshoo M,
Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; SEQ ID NO 106; 194pp; English
                                ADES2068 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eirich LD,
Loper JC, (
                                                                                                                                                                                                                                                                                                                                                          05-0CT-1998; 98US-0103099P.
10-MAR-1999; 99US-012355P.
30-APR-1999; 99US-00302620.
12-0CT-2001; 2001US-00976800.
                                                                                                                                                                                                                                                                                                              03-MAY-2002; 2002US-00138916
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson CR, Craft DL,
Brenner AA, Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-625522/59
                                                                                                                                                                                                                                                                                                                                                                                                                                            WILSON C R.
                                                                                                                                                                                                              Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYP or CPR genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 267 AA;
                                                                                                                                                                                                                                            US2003073220-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADE52067
                                                                                                                                                                                                                                                                                                                                             01-MAY-1998;
                                                                                              29-JAN-2004
                                                                                                                                                                                                                                                                             17-APR-2003
                                                                ADE52068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BREN/)
(TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EIRI/)
(ESHO/)
(MADD/)
(CORN/)
RESULT 8
                  ADE52068
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0; Gaps

Score 19; DB 7; Length 267; Pred. No. 1.8e+03; 0; Mismatches 3; Indels

86.4%;

Query Match
Best Local Similarity 57.1
Matches 4; Conservative

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                                                                                                                                                                                                                                                                                                                              CYP52A2B; cytochrome P450; NADH reductase; dicarboxylic acid production; organic substrate oxidation; fatty acid oxidation; gene integration vector; CYP; CPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding a CYP52A2B protein useful for increasing the production of dicarboxylic acid for oxidizing organic substrates such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid encoding a CYP52A2B protein comprising the fully defined sequence of 522 amino acids, as given in the specification, and comprising a coding region defined by nucleotides 1072-2640 of a fully defined sequence of 3755 base pairs, given in the specification. The nucleic acids encoding the cytochrome P450 and NADH reductase enzymes of Candida tropicalis are useful for increasing the production of dicarboxylic acid for oxidising organic substrates such as fatty acids. This sequence represents a Candida tropicalis associated polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madduri KM,
                                                                                                                                                                                                                                                                                      Candida tropicalis associated polypeptide seg id 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eirich LD, Eshoo M, oper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 106; 188pp; English.
                                                                                                                                                     ADF72375 standard; protein; 267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loper JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001US-00976800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0123555P
                                                                                                                                                                                                                                              12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILSON C R.
CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-810780/76
                                          45
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LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           Candida tropicalis
1 VXXXAEF
                                       39 VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS2003077795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BREN/)
(TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MADD/)
(CORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (/STIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESHO/)
                                                                                                           RESULT 9
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RESULT 10 ADF11815

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The invention relates to a new isolated nucleic acid which encodes a CPRA, CPRB, CYP52A1A, CYP52A2B, CYP52A3B, CYP52A3B, CYP52A8B, CYP52A8B, CYP52A8B, CYP52A8B or CYP52D4A protein. The nucleic acid is useful for discriminating between members of a gene family by quantifying the amount of mRNA in a sample. The present sequence represents the aminacid sequence of a Candida tropicalis protein.
                                                                       CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5A, CYP52A5A, CYP52A8B, CYP52D4A, gene family, URA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A6B or CYP52D4A gene, useful for discriminating members of a gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 7; Length 267;
Pred. No. 1.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Madduri KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integration vector pURA2in URA3A gene encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΣΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 106; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Eshoo M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eirich LD,
Loper JC, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE64232 standard; protein; 267
                                                                                                                                                                                                                                           01-MAY-1998; 98US-0083798P.
05-OCT-1998; 98US-0103099P.
10-MAK-1999; 99US-0123555P.
310-APR-1999; 99US-0030520.
12-OCT-2001; 2001US-00976800.
                                                                                                                                                                                                                   03-MAY-2002; 2002US-00139296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 86.4%;
Similarity 57.1%;
4; Conservative (
            12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                    MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                      CRAFT D L.
EIRICH L D.
ESHOO M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-897579/82
                                        C. tropicalis URA3A
                                                                                                                                                                                                                                                                                                                                           WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                        Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADF11696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 267 AA;
                                                                                                                                                     US2003148486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                    07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE64232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                           (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                       (MADD/)
(CORN/)
(BREN/)
                                                                                                                                                                                                                                                                                                                                                                          EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                        ESHO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a new isolated nucleic acid which encodes a CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3B, CYP52A5B, CYP52A5B, CYP52A6B or CYP52D4A protein. The nucleic acid is useful for discriminating between members of a gene family by quantifying the amount of mRNA in a sample. The present sequence represents the amino acid sequence of a Candida tropicalis protein.
                                                                                                                                                   CPRA; CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A; CYP52A5B; CYP52A5B; CYP52A5B; CYP52D4A; gene family; URA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A5B, CYP52A5B, CYP52D4A gene, useful for increasing production of dicarboxylic acid.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%; Score 19; DB 7; Length 267; 57.1%; Pred. No. 1.8e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Madduri KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eirich LD, Eshoo M,
Loper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 106; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF11697 standard; protein; 267 AA.
                           ADF11815 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                      01-MAY-1998; 98US-00083798P.
05-OCT-1998; 98US-0103099P.
10-MAR-1999; 99US-0013555P.
30-APR-1999; 99US-00302620.
12-OCT-2001; 2001US-00976800.
                                                                                                                                                                                                                                                                                            03-MAY-2002; 2002US-00139218.
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                 CRAFT D L.
EIRICH L. D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-897719/82
                                                                                                                        C. tropicalis URA3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITTAEF 45
                                                                                                                                                                                                  Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                      WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADF11814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 267 AA;
                                                                                                                                                                                                                                US2003153060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brenner AA,
                                                                                       12-FEB-2004
                                                                                                                                                                                                                                                               14-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                          ADF11815;
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(CRAF/) (EIRI/) (ESHO/) (MADD/)

(MILS/)

(CORN/) (BREN/) (TANG/) (LOPE/)

Cornett CA;

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Gaps

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Query Match

Matches

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ADF11697

RESULT 11
ADF11697
ID ADF11
XX
AC ADF11

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The present sequence is that of the polypeptide encoded by the URAJA selectable marker gene of Candida tropicalis. A claimed C. tropicalis cell has a disrupted chromosomal POX4 and/or POX5 gene in which a portion of the gene(s) is deleted through homologous recombination with a selectable marker gene, especially URAJ. This blocks the beta-oxidation pathway of the cell. The size of the deletion of the chromosomal gene prevents the strain from reverting to wild-type activity. The cell is used in a claimed process for producing alpha,omega-dicarboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-revertible beta-oxidation blocked Candida tropicalis cell having a disrupted chromosomal POX4 and/or POX5 gene(s), useful for producing dicarboxylic acids used in the preparation of perfumes or macrolid antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP; CPRA protein; CPRB protein; dicarboxylic acid; plastic; adhesive;
fragrance; URAJA.
                                                                                                                            JRA3; selectable marker; enzyme; beta-oxidation; dicarboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h Similarity 57.1%; Pred. No. 1.8e+03; Indels 64; Conservative 0; Mismatches 3; Indels 65
                                                                           Candida tropicalis URA3 gene-encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 10; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ26614 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida tropicalis URA3A protein.
                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2002; 2002US-0383332P.
                                                                                                                                                                                                                                                                                                                              22-MAY-2003; 2003WO-US016453
                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2003; 2003US-0044467
                            11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-081907/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COGN-) COGNIS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                           Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 VITTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADG73845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 267 AA;
                                                                                                                                                                                                                            WO2003100013-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003186411-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-2004
                                                                                                                                                                                                                                                                             04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craft DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ26614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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ADJ26614
     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated CPRA, CPRB, CYP52A1A, CYP52A2A,
CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5B, CYP52A1B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A4 protein (CYP-cyptochrome P450, CPR - NADPH reductase) of the Candida tropicalis omega-hydroxylase complex. Also included are the nucleic aids encoding the CYP/CPR proteins (including their coding capins), a vector comprising the nucleotide acid, a host cell transfected or transformed with the vector, discriminating members of a gene family by quantifying the amount of target manA in a sample and increasing production of a dicarboxylic acid (comprising: providing a host cell having a naturally occurring CPR/CYP protein and culturing the host cell having an organic substrate which upregulates the core of the containing an organic substrate which upregulates the core of the containing an organic substrate which upregulates the core of the containing an organic substrate which upregulates the core of the containing an organic substrate which upregulates the core of the containing and containing contain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5B, CYP52A6B or CYP52D4A protein, useful for increasing production of dicarboxylic acid in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madduri KM, Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 8; Length 267; Pred. No. 1.8e+03; 0; Mismatches 3; Indel8
Yeast; enzyme; NADPH reductase; CPR; cytochrome P450; CYP; omega-hydroxylase; dicarboxylic acid; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eirich LD, Eshoo M, oper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; SEQ ID NO 106; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loper JC,
                                                                                                                                                                                                                                                                     01-MAY-1998, 98US-0083798P.
05-0CT-1998, 98US-0103099P.
10-MAK-1999, 99US-0123555P.
30-APK-1999; 99US-0030520.
12-0CT-2001, 2001US-00976800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%;
57.1%;
                                                                                                                                                                                                                         03-MAY-2002; 2002US-00138905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson CR, Craft DL,
Brenner AA, Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-020205/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integration vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 VTTTAEF 45
                                                                                                                                                                                                                                                                                                                                                                                                                            WILSON C R.
                                                                           Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE64231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 267 AA;
                                                                                                                         US2003068800-A1
                                                                                                                                                                        10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                         (WILS/)
(CRAF/)
(EIRI/)
(ESHO/)
(MADD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORN/)
(BREN/)
(TANG/)
(LOPE/)
(GLEE/)
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Gaps

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03-APR-2003; 2003US-00405660.

ADG73846 standard; protein; 267 AA.

RESULT 13 ADG73846 ID ADG7 XX AC ADG7

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ADG73846

PRESENTATION OF STREET OF

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
                                                                                     Candida tropicalis transformation system - using host auxotrophic in an amino acid, purine or pyrimidine pathway as result of mutagenesis.
                                                                                                                                                                  The gene product ( and opt. the URA3 A gene product - AAR06639) is used to complement an auxotrophic host to prototrophy. The host may be defective in orotidine-5'-phosphate decarboxylase activity. See also AAQ05864-Q05866
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                   86.4%; Score 19; DB 2; Length 268;
57.1%; Pred. No. 1.8e+03;
ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli cellular proliferation protein #230.
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      ŝ
      Picataggio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU34649 standard; protein; 298 AA.
                                                                                                                                     Disclosure; Fig 4; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
22-NOCY-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0253931P.
16-FEB-2001; 2001US-0269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                   Local Similarity 57.1
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     Gleeson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611495/70.
N-PSDB; AAS52508.
                                     WPI; 1990-275138/36.
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                                                                                                                                                                                                                                                                                                                                                    1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                   39 VTTTAEF
                                                     N-PSDB; AAQ05865
                                                                                                                                                                                                                                                      Sequence 268 AA;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002
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     Cregg JM,
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                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises CYP genes from Candida tropicalis which encode CPRA and CPRB proteins. The invention is useful for CPRA and CPRB protein production, the DNA and protein sequences are useful for increasing production of dicarboxylic acid in chemical products, such as: plastics, adhesives and fragrances. The present amino acid sequence represents a Candida tropicalis URA3A protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding a CPRA protein, used to increase production of dicarboxylic acid, for use in chemical products including plastics, adhesives, and fragrances.
                                                                                                                                                                                                                                                                                     Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uracil biosynthetic pathway; orotidine-5'-phosphate decarboxylase;
URA3 B gene; auxotrophe; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orotidine-5'-phosphate decarboxylase encoded by the URA3 B gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%; Score 19; DB 8; Length 267; 57.1%; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                   Madduri KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                   , Eshoo M,
Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 106; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR06640 standard; protein; 268 AA.
                                                                                                                                                                                                                                                                                   Eirich LD,
                                                                                                                                                                                                                                                                                                      Loper JC,
01-MAY-1998; 98US-00083798P.
05-OCT-1998; 98US-0103099P.
10-MAR-1999; 99US-0123555P.
30-APR-1999; 99US-0030520.
12-OCT-2001; 2001US-00976800.
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89US-00386837
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Les 4; Conservative
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                                                                                                                                                                                                                                                                                   Craft DL,
Tang M,
                                                                                                                                EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                   WPI; 2004-088917/09.
                                                                                                     WILSON C R.
                                                                                                                                                                                                                TANG M.
LOPER J C.
GLEESON M.
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                                                                                                                    CRAFT D L.
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                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADJ26613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 267 AA;
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27-JUL-1989;
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                                                                                                                                                                                                                                                                                   Wilson CR,
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                                                                                                                                                                                (CORN/)
(BREN/)
(TANG/)
(LOPE/)
                                                                                                                  (CRAF/)
(EIRI/)
(ESHO/)
(MADD/)
                                                                                                   (MILS/)
                                                                                                                                                                                                                                                   (GLEE/)
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Matches
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             useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a rokariety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell contraining the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding
Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
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Xu HH;
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0
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #14234.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 56631; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU28707 standard; protein; 298 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
06-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                    86.4%;
57.1%;
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                               172 VSTTAEF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-029926/02
                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                                    Sequence 298 AA;
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Wall
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
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                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 6; Length 298; Pred. No. 2e+03; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 298 AA;
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11) The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed care in diagnostics as expressed sequence tags for identifying expressed care in diagnostics as expressed sequence tags for identifying expressed care in diagnostics in serving antibodies states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and anno acid sequences. Assolotto-Assolator responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Assolotto-Assolator responsible for genetic distribution. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the inventores.
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invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%; Score 19; DB 4; Length 305; 57.1%; Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW69244 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour inhibitor; clone CK201 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone CK201_1 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US023224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00766263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00989232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.1 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 VSTTÄEF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-362424/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV44863
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-1996;
11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9825962-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW69244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  е.
9
                                           This sequence is secreted protein, encoded by a polynucleotide of the invention. The DNA was isolated from a human adult testis cDNA library, and is designated clone CK201 1. The DNA sequences and encoded polypeptides can be used as nutritional sources or supplements, or may exhibit e.g. cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity, activity, chemostatic/chemokinetic activity, cadherin/tumour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids encoding polypeptides, useful for modulating e cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans C;
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Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                     Score 19; DB 2; Length 309;
Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CK201_1 protein sequence SEQ ID 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 473-474; 557pp; English.
                 Claim 27; Page 74-75; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB90724 standard; protein; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000; 2000WO-US025135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00398829.
                                                                                                                                                                                                                                                                                       86.4%;
57.1%;
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                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  275 VSAAAEF 281
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF 7
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                                                                                                                                                                                                                                                     Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haematopoiesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB90724;
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Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are: (1) a vector comprising a promocer operably linked to the nucleic acid mucleic acid. (2) a host cell containing the vector; (3) an isolated polypeptide whose expression is inhibited by the antisense antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies
chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; haematopoiesis activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the CDNA clones encoding the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                          Gaps
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                                                                                                                 Length 309;
                                                                                                                                          3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #30241.
                                                                                                               Score 19; DB 4; I
Pred. No. 2.1e+03;
); Mismatches 3;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 72638; 1766pp; English.
                                                                                                                                                                                                                                                       ABU44714 standard; protein; 338 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                  Salmonella paratyphi
                                                                                                                                                                                          275 VSAAAEF 281
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                                                                                                                                                                   7
                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                   1 VXXXAEF
                                                                                        Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACA48584
                                                                                                                                                                                                                                                                                                                                                                                                           WO200277183-A2
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                                                                                                                                          4;
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                                                                 proteins
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Wall D,
                                                                                                                                        Matches
                                                                                                                                                                                                                                RESULT 21
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                       organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in a electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy,
proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 338;
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Pred: No. 2.3e+03;
0; Mismatches 3; Indels
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Otsuki
   gene on which the test compound that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K, Sa
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:12146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB93191 standard; protein; 697 AA.
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Sugiyama T, Wakamatsu
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99JP-00300253.
2000JP-00118776.
2000JP-00183767.
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Local Similarity 57.1%;
Les 4; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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11-JAN-2000;
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB93191;
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of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5-end sequence and an oligonuclectide comprising a sequence complementary to the sequence and an oligonuclectide comprises a 3'-end sequence, where the polynuclectide which comprises a 1'-end sequence, where the oligonuclectide which comprises a 1'-end sequence, where the combination of the 5'-end sequence, as selected from those defined in the specification. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the compranding of the full-length cDNAs. The primers are also useful for the companion and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs and 13'-end sequences; AAH13612 represent thuman amino acid sequences; and AAH1362 represent consideration of the companion of the companio
      oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 697 AA;
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Score 19; DB 4; Length 697; Pred. No. 5.1e+03; 0; Mismatches 3; Indels 86.4%; 57.1%; Ouery Match
Best Local Similarity 57.1.
67.1. 662 VSAAAEF 668 ۲ 1 VXXXAEF ð 유

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Gaps

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ADL90006 standard; protein; 957 AA. (first entry) 20-MAY-2004 ADL90006; RESULT 23 ADL90006 

transaldolase activity; glucose-6-phosphate isomerase; NADH production; target substance manufacture; enzyme; glucose-6-phosphoric acid isomerase. Gluconobacter oxydans glucose-6-phosphoric acid isomerase protein.

Gluconobacter oxydans

JP2004024140-A.

29-JAN-2004.

26-JUN-2002; 2002JP-00186487

26-JUN-2002; 2002JP-00186487.

(AJIN ) AJINOMOTO

N-PSDB; ADL90004

WPI; 2004-127093/13.

Novel protein having transaldolase activity or glucose-6-phosphate isomerase activity, useful for producing a target substance e.g., Claim 1; SEQ ID NO 18; 89pp; Japanese. xylitol.

The invention comprises the amino acid and coding sequences of dluconobacter oxydans proteins which possess transationaes activity and/or glucose-6-phosphate impenses activity. The DNA and protein sequences of the invention are involved in the production of NADH. The DNA and protein sequences of the invention are useful for manufacturing a target substance. The present amino acid sequence represents the Gluconobacter oxydans glucose-6-phosphoric acid isomerase protein.

Sequence 957 AA;

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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular confiferation or the activity of a gene in an operon required for proliferation, (7) identifying a gene product or that has an activity against a biological pathway confirmed for proliferation, (7) identifying a campound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits profiling a compound; sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; or the inhibits the compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying the tast of the acids are useful for identifying the tast of the acids are useful for identifying the tast of the product is acids are useful for identifying the tast of the product is acids are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense, prokaryotic essential gene, cell proliferation, drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                     Gaps
                                                                     ö
                    Length 957;
                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #33272.
                    Score 19; DB 8; I
Pred. No. 7.2e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 75669; 1766pp; English.
                                                                                                                                                                                                                                                                       ABU47745 standard; protein; 1266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
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                       86.4%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                           (first entry)
Query Match
Best Local Similarity 57.1.
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                           861 VATAAEF 867
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                                                                                                            1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmomella typhi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                                                                 ABU47745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang L,
Wall D,
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               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at firm wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antiarteriosclerotic; cerebroprotective; antiparkinsonian; anticonvulsant; anti-HIV; antiallergic; antibacterial; virucide; gene therapy; nucleic acid-associated protein; cancer; atherosclerosis; stroke; Parkinson's disease; epilepsy; Cushing's syndrome; AIDS; allergy; microarray element; protein protein interaction; drug-target interaction; gene expression; chromosomal mapping; diagnosis.
cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee SY, Marquis JP;
Warren BA, Yang J;
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wla NK, Elliott VS;
Gorvad AE, Griffin JA;
                                                                                                                                                                                                                     ö
                                                                                                                                                                                 Length 1266;
                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emerling BM, Forsythe IJ, Gietzen KJ, Gorvad Al
Hafalia AJA, Ison CH, Lal FG, Lee EA, Lee S,
Ramkumar J, Sprague WW, Swarnakar A, Tang YT,
Yue H, Zebazjadian Y,
                                                                                                                                                                                 86.4%; Score 19; DB 6; I
57.1%; Pred. No. 9.9e+03;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burford N, Chawla NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human nucleic acid-associated protein #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 7; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                       ADJ80131 standard; protein; 1450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001; 2001US-0335544P.
05-NOV-2001; 2001US-0337535P.
09-NOV-2001; 2001US-0344650P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2001; 2001US-0344650P
15-NOV-2001; 2001US-0334762P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001US-034842P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2002; 2002WO-US034846
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                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004 '(first entry)
                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                    895 VSSSAEF 901
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                                                                                                                                                                                                                                                   1 VXXXAEF 7
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                   Seguence 1266 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003038052-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2003
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                      RESULT 29
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The invention relates to novel human nucleic acid-associated proteins and genes encoding them, sequences that have at least 90-99 % identity to the sequences, or biologically active or immunogenic fragments of these. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing disorders associated with aberrant expression of NAAP, such as

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cell proliferative (e.g. cancer or atherosclerosis), neurological (e.g. stroke, Parkinson's disease or epilepsy), developmental (e.g. Cushing's syndrome), autoimmune/inflammatory (e.g. AIDS or allergies), or infections. These may also be used as elements on a microarray which may monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles. The polynucleotide may also be used in chromosomal mapping and in various diagnostic assays. These are also useful in assessing the effects of exogenous compounds on the expression of mucleic acids and amino acid sequences of NAAP, in facilitating discovery process, and in investigating the pathogenesis of diseases or medical conditions. This sequence corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic, antirheumatic, antiarthritic; antidiabetic; ophthalmological; antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis; gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; ischemic limb disease; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of novel genes (ACF3446-ACF34559) encoding proteins (ABR64100-ABR64281) involved in the process of angiogenesis. The nucleic acid molecules are useful in identifying and/or obtaining full-length human genes involved in an angiogenic process. The
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New angiogenic genes and polypeptides, useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis
                                                                                                                                                                                                                                                                     86.4%; Score 19; DB 7; Length 1450; 57.1%; Pred. No. 1.1e+04; ive 0; Mismatches 3; Indel8
                                                                                                                                                                                                 to one of the proteins of the inventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 173; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR64238 standard; protein; 1584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001AU-00007973.
2001AU-00007974.
2001AU-00008210.
2001AU-00008532.
2001AU-00008838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vadas MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2002; 2002WO-AU001282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002AU-00951032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenesis protein BNO147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                1415 VSAAAEF 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-354655/33.
N-PSDB; ACF34513.
                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                      Sequence 1450 AA;
                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001;
27-SEP-2001;
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29-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR64238;
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
ABR64238
       88888888888888888888
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for expression of a polynucleotide encoding a polypeptide from a

microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant

combinant DNA construct and growing transforming a plant with the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for producing plant properties.

The recombinant DNA construct is useful for producing plant with construct is useful for producing plant properties.

The recombinant DNA construct is useful for producing plants with concreased resistance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and estenoment and production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form at the printed specification but was obtained in electronic forms.

format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 2214 AA;

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controlled acid molecule, polypeptides or complexes encoded, cells or genetically modified non-human animals derived from these are useful for the screening of candidate plaramaceutical compounds used in treating angiogenesis-related disorders. They are also useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, which involves uncontrolled or enhanced angiogenesis or is a disorder; which involves uncontrolled or enhanced angiogenesis or is a disorder in which a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis, atherosclerosis), or involves inappropriately arrested or decreased angiogenesis or is a disorder in which an expanding vasculature is of benefit (e.g. ischemic limb disease or coronary artery disease). The modulator of expression or activity of the polypeptide encoded by the couleic acid sequence is useful for manufacturing a medicament for the treatment of an angiogenesis-related disorder. This sequence corresponds to one of the novel angiogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; brethicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 19; DB 6; Length 1584; 57.1%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003233675-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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I 10 ADNIZ 4084

XXX ADNIZ ADN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                                                                                                                                                           Human; memapsin 2; aspartic protease; beta secretase;
degenerative disease; Alzheimer's disease; amyloid precursor protein;
APP; neuroprotective; nootropic; inhibitor;
                        Gaps
                          ö
86.4%; Score 19; DB 8; Length 2214; 57.1%; Pred. No. 1.8e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                      Memapsin 2 substrate specificity determination peptide #30
                                                                                                                                                                                                                                                                                                                                                                                                                                    (OKLA-) OKLAHOMA MEDICAL RES FOUND
                                                                                                                                 ABG78424 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 52; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ghosh AK;
                                                                                                                                                                                                                                                                substrate side-chain preference
                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                          28-DEC-2001; 2001WO-US050826
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                                                                                                                                                                               (first entry)
                          4; Conservative
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                                                                       1770 VITSAEF 1776
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                                                1 VXXXAEF 7
            Local Similarity
                                                                                                                                                                                                                                                                                                                          WO200253594-A2.
                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                               15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                   11-JUL-2002.
                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                        ABG78424;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease
              Best Loca
Matches
                                                                                                                                                                                                                                                                                         Homo
                                                                                                          RESULT 28
                                                                                                                     ABG78424
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Goldman BS;

Chen X,

Hinkle GJ, Slater SC,

Cao Y,

WPI; 2004-061375/06.

HINKLE G J. SLATER S C. CHEN X. GOLDMAN B S.

(CAOY/)

(CHEN/)

(SLAT/) (HINK/)

20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to

SEQ ID NO 6737; 122pp; English.

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The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is a method of determination of the substrate binding cleft. Also included is commapsin 2 sub-sites comprising; (a) reacting a mixture of memapsin 2 and determining the sub-site preference of memapsin 2 by determining relative initial hydrolysis rates of the continuary of memapsin 2 inhibitors containing a base sequence taken from Compassin 2 inhibitors containing a base sequence taken from Compassin 2 inhibitors containing a base sequence taken from Compassin 2 inhibitors with memapsin 2 which binds to several inhibitors to generate several bound memapsin 2, and detecting the bound memapsin 2 with an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a containing the substrate side-chain preference in memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP). Depting the present sequence represents a substrate in the cleavage of amyloid precursor protein (APP) sub-sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, memapsin 2, aspartic protease, beta secretase,
degenerative disease, Alzheimer's disease, amyloid precursor protein,
APP, neuroprotective, nootropic, inhibitor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Memapsin 2 substrate specificity determination peptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                 determine the substrate specificity of human memapsin 2
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 5; I
Pred. No. 1.2e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG78419 standard; peptide; 12 AA.
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14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
57.1%;
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Best Local Similarity
4, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-619088/66
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
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binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is a method of determination of the substrate side-chain preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 substrates with memapsin 2, and determining the sub-site preference of memapsin 2 by determining relative initial hydrolysis rates of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial intravers of memapsin 2 substrates; or (b) preparing a combinatorial intravers of memapsin 2 inhibitors containing a base sequence taken from OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for the present sequence represents a substrate in memapsin 2 sub-sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzheimer's disease; amyloid precursor protein; APP; neuroprotective; nootropic; inhibitor; substrate side-chain preference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Memapsin 2 substrate specificity determination peptide #24.
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0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                              determine the substrate specificity of human memapsin
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(UNII ) UNIV ILLINOIS FOUND.
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14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001WO-US050826
                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-619088/66.
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Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
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memapain 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 substrates with memapsin 2, and determining the sub-site preference of memapsin 2 by determining relative initial hydrolysis rates of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial library of memapsin 2 inhibitors containing a base sequence taken from (oM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 which binds to several inhibitors to generate several bound memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (App), and for determining the substrate side-chain preference in memapsin 2 sub-sites.

The present sequence represents a subsite variant peptide used to
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                                                                                                                                                                                                                                                                                                               Gaps
determination of the substrate side-chain preference in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipoprotein; E.coli outer membrane protein (OMP) A signal peptide.
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                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                               3; Indels

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/label= signal peptide/ protein junction
                                                                                                                                                                                                                        determine the substrate specificity of human memapsin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMP A-2 signal peptide/heterologous protein junction.
                                                                                                                                                                                                                                                                                                .2e+02;
                                                                                                                                                                                                                                                                                Score 18; DB 5;
Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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84US-00607224.
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57.1%;
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Best Local Similarity 57.1.
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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                                                                                                                                                                                                                                                                                                                                                                         VNSAAEF 12
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                                                                                                                                                                                                                                                                                                                                           1 VXXXAEF
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                                                                                                                                                                                                                                                      Sequence 12 AA;
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method of
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Efficiency of expression of lipoprotein expression vectors is improved by introducing the omp A signal peptide from E.coli in place of lipoprotein signal sequence. A fusion protein is produced where the desired protein carries the omp A signal peptide at its N-terminal end. This signal

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The invention relates to annotating a query sequence involving accessing patterns associated with a database comprising annotated sequences, assigning attributes to the patterns based on the annotated sequence assigning attributes to the patterns based on the annotated sequence and using the patterns with assigned attributes to analyse the query sequence. Also included are an apparatus for annotating a query sequence. The method further comprises the step of selecting the accessed patterns that match the query sequence, storing the patterns with assigned attributes, the attribute vector from the patterns with assigned attributes, the attribute vector from the patterns with assigned attributes, the attribute vector comprises a number of counters of the query sequence is a polypeptide sequence comprising amino acid residues and the attribute vector comprises a number of counters (the number of counters of the assigned attributes are used to contribute values to counters of the assigned attribute vector corresponding to portions of the query sequence matched by the patterns. The method also comprises a plurality of attribute vectors where the plurality of
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            is then cleaved off. No modification of the cleavage site is necessary during the secretion process, unlike for the lipoprotein signal peptide. Synthetic linkers were inserted to ensure the structural gene was in phase with the signal sequence. Proteins encoded by plasmids omp A-1 and omp A-3 demonstrate the other two reading frames. (AAN80124 and AAN80126). See also AAN80118-9 and AAN80128. (Updated on 25-MAR-2003 to correct PA field.)
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translocation of the product across the cytoplasmic membrane and
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ubiquitin, annotated sequence, query sequence, database, secondary structure characteristic, bio-dictionary.
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                                                                                                                                                                                                                         Score 18; DB 1; Length 13; Pred. No. 1.3e+02; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO52379 standard; peptide; 41 AA.
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                                                                                                                                                                                                                         81.8%;
57.1%;
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                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ubiquitin peptide
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                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                   Sequence 13 AA;
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  directs
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Matches
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disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle disorders

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attribute vectors are ranked, and the top ranking attribute vectors are reported. The method comprises the step of determining a score for the patterns with assigned attributes used to contribute to the attribute vector. The score represents a degree of similarity between the query sequence and the annotated sequences of the database and the score is normalised. The attributes relate to at least one of secondary structure characteristics of the query, presence of known domains, signal peptides, active sites, post-translationally modified sites, cytoplasmic behaviour, extracellular behaviour, and similarity of the query to each of the three phylogenetic domains as a function of amino acid position. The method is
                                                                                                                                                                                             used for analysing or annotating query sequence e.g. protein or amino acid sequence, for elucidating properties of protein (including functional, structural and physiochemical properties) directly from corresponding amino acid sequence and for forming a bio-dictionary. The method is also useful for determining cytoplasmic, transmembrane or extracellular region of a query sequence and allows automated elucidation for annotating query sequences or complete genomes, quickly, exhaustively and objectively and avoids tedious manual analysis as reported previously. The present sequence is a peptide from human ubiquitin, analysed using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 81.8%; Score 18; DB 8; Length 41; Local Similarity 57.1%; Pred. No. 4.5e+02; les 4; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB61451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61451
    $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.
                                                                                                                                                                                                                                                                                                                                                             Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                  Modular enzyme system related ACP-domain N-terminal peptide MTAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 5; Length 47;
Pred. No. 5.3e+02;
0; Mismatches 3; Indels
                                                                                   Length 44
                                                                                Score 18; DB 4; ]
Pred. No. 4.9e+02;
0; Mismatches 3
                                                                                                                                                                                                                                              AAM47175 standard; peptide; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 9; 83pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ACTI-) ACTINODRUG PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2000; 2000DE-01021267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2001; 2001WO-DE001578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                  81.8%;
57.1%;
                                                                  Query Match
Best Local Similarity 57.10,
                                                                                                                                                                                                                                                                                                       12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Stigmatella aurantiaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-049276/06
                                                                                                                                                                       35 VYSSAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSALAEF 42
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                                                                                                                                          1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47 AA;
                                                        Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200181564-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schauwecker F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                           AAM47175;
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                                                                                                                                                                                                                   RESULT 34
                                                                                                                                                                                                                                  AAM47175
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AAY14477 standard, protein; 56 AA.
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                                                                                                                                                                                                                                                     WO9919339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Florence KA,
                                                                                                                                                                                                                                                                                                         08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-1997;
                                                    17-AUG-1999
                                                                              Fragment of
                                                                                                                                                                                                                                                                              22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                  09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loci
Matches
The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or cageneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
                                                                                                                                           myeloid cell disorder; lymphoid cell disorder;
bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                       , Wang J;
Wang D;
                                                                                                                                forensic; nutritional source; damaged tissue; diseased tissue;
                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 18; DB 7; Length 53; 57.1%; Pred. No. 6e+02; 1ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 957; 156pp; English.
                        ADI21706 standard; protein; 53 AA
                                                                                                      Novel human polypeptide #185.
                                                                                                                                                                                                                                                                                          19-SEP-2002; 2002WO-US029964.
                                                                                                                                                                                                                                                                                                                     19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739.
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-354603/33.
N-PSDB; ADI21486.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                       WO2003025148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53 AA;
                                                                                                                                                                                                              Homo sapiens.
                                                                            15-APR-2004
                                                                                                                                                                                                                                                                27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide
                                                   ADI21706;
RESULT 35
             ADI21706
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This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX19012) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 53 novel genes and their fragments (nucleic acid sequences: AAX19011-X79064; amino acid sequences AAX19011-X19464) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 53 polymucleotides, based on which tissues they are most highly expressed in (see AAX79011 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; observine; arthritis; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrie AM, Florence C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode.
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Pred. No. 6.4e+02;
0; Mismatches 3; Indels
                                                           human secreted protein encoded by gene 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ian R, Ebner R, Re
Greene JM, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 14; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ12304 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0061527P.
97US-0061529P.
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97US-0061536P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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4; Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-277587/23.
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Best Local Similarity
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Gaps ö

27 VRTSAEF 33

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RESULT 36 AAY14477

1 VXXXAEF 7

Matches

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nument, becare of carbonic frame accorder; prostatitis;

nument, becare of carbonic frame accorder; prostatitis;

multiple myeloma; reproductive system disease; systemic lupus erythematosus;

muguinal hernia; musculoskeletal disease; systemic lupus erythematosus;

mout, cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;

mouther alcohol syndrome; Down's syndrome; excretory disease;

morphimer's disease; meningitis; respiratory disease; emphysema;

morphimer's disease; meningitis; respiratory disease; emphysema;

morphimer's disease; endocrine disease; endoral hypertension;

morphimer's disease; endocrine disease; scleroderma;

glomerulonephritis; digestive disease; portal hypertension;

mritable bowel syndrome; epithelial disease; scleroderma;

antiathmatic; antihacterial; osteopathic; dermatological; antigout;

antisathmatic; antibacterial; osteopathic; dermatological; antigout;

mingunomodulator; antiarrhythmic; cardiant; nootropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;

methrotropic; uropathic; hypertensive; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Florence KA, Gre
Ebner R, Olsen H;
                                                                                secreted; cancer; haematopoietic disease; anaemia;
                                                      Peptide feature of a human secreted protein SegID 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duan RD, Ruben SM,
Yu G, Florence C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 158; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0061527P.
97US-0061529P.
97US-0061532P.
97US-0061536P.
97US-0071498P.
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99US-00288143
2000US-0244591P
                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-2001; 2001US-0098429
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLORENCE K A. GREENE J M. YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brewer LA,
Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-090518/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BREWER L A.
DUAN R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLORENCE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN C A.
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OLSEN H.
                                                                                                                                                                                                                                                                                                                                                  US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-0CT-1997;
09-0CT-1997;
09-0CT-1997;
09-0CT-1997;
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2000;
                           20-MAY-2004
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Young PE,
 ADJ12304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YUGG/)
(FLOR/)
(EBNE/)
(OLSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BREW/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOUN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUAN/
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This invention relates to novel polynucleotides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or

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preventing disorders such as cancer, haematopoietic diseases including anaemia and multiple myeloma, reproductive system disorders including prostatitis and inguinal hernia, musculoskeletal diseases including systemic lupus erythematosus and gout, cardiovascular diseases including arrhythmia and hypernatraemia, mixed fetal diseases including fetal alcohol syndrome and Down's syndrome, excretory diseases including alcohol syndrome and Down's syndrome, excretory diseases including curinary incontinence and renal disorders, neural or sensory disease including alabetes and glomeralonephritis, disease, endocrine diseases including emphysema and occupational lung disease, endocrine diseases including portal hypertension and irritable bowel syndrome and connective tissue or epithelial diseases including scleroderma and epidermolysis bullosa. As such, there are various activites such as cytostatic, antianemic, antiathmitic, antistathmatic, antistathmatic, antistathmatic, antistathmatic, antistation, and a feature of a human secreted protein of the invantion. NoTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the US patent office at the following web site

"Www.seqdata.uspto.gov/sequence.html; Document ID: 20040010132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel testes-specific gene 22P4F11 which is expressed in human prostate cancer and is useful as a diagnostic marker and/or therapeutic target for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22P4F11; human; testis; prostate cancer; diagnosis; therapy; marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 8; Length 56;
Pred. No. 6.4e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human testis-specific 22P4F11 partial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY79490 standard; protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afar DE, Hubert RS, Mitchell SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
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99US-0146584P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFAR D E.
HUBERT R S.
MITCHELL S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-303452/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 VAARAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ94894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200018925-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY79490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
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RESULT 40
ADB09905
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                          The present sequence is that of a human 22P4F11 polypeptides, as deduced from an isolated partial CDNA (see AAZ94894). The full-length 22P4F11 sequence is provided in AAY79489. 2224F11 is a testis-specific gene in normal tissues, and is also expressed in human prostate tumours, in some cases at high levels. The 22P4F11 transcript and/or protein may represent a useful diagnostic marker and/or therapeutic target for prostate cancer. Methods of using 22P4F11 polynucleotides, polypeptides and antibodies for the diagnosis and treatment of cancers expressing 22P4F11, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                       Score 18; DB 3; Length 69;
Pred. No. 8.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 12892; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX protein sequence SEQ ID NO:12892.
                                                                                                                                                                                                                                                                                                                                                                                                                ABP06455 standard; protein; 73 AA.
Example 1; Fig 1B; 54pp; English.
                                                                                                                                                                                                                                         81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US010836.
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                            development of such cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                        Local Similarity 42.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                  ISTTAEF 7
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                                                                                                                                                                                                                                                                                                      1 VXXXAEF
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                                                                                                                                                                                                          Sequence 69 AA;
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syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, cateoarthritis, neurodegenerative disorders, disorders, haemorrhage, cransplantarion, cardiovascular diseases, disbetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester atorage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatosid arthritis, autoimmune thyroidits, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bene degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from content of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I) an isolated polypetide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, degenerate variant or fragment; (3) a genetically engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 5; Length 73; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zagursky RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alloiococcus otitis antigenic protein SEQ ID NO:3718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fletcher LD, Mcmichael JC, Russell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB09905 standard; protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
57.1%;
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18-NOV-2002; 2002US-0426742P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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N-PSDB; ADB09908.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 73 AA;
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host cell, transfected, transformed or infected with the vector of (2);

(4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polymorlectide that is comprised in the expression vector; (6) a pharmaceutical composition comprising the polypeptides of (1) and a carrier; (7) a protein chip comprising the polypeptides of (1), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus ortitidis in the biological sample; (10) a kit comprising a container containing the novel polymuclectide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the polymetically enginerated host cell under conditions suitable to produce the polypeptide from the culture. (1) can be used in gene therapy. The polymuclectides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials. The present sequence represents an Alloiococcus otitidis and the present sequence represents an Alloiococcus otitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; hitrogen; phosphorus; photosynthesis; lignin; galactomannan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 6; Length 83; 57.1%; Pred. No. 9.9e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                   antigen protein from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS21033 standard; protein; 93 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial polypeptide
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GOLDMAN B S.
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SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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ADS21033
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promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant combinant DNA construct and growing the transformed plant, where the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with inproved plant properties, e.g. improved cold, heat or drought tolerance, collerance to herbicides, extreme semotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved ylelad by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and envelopment under at least one stress condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 93;
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57.1%; Pred. No. 1.18+03;
.ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       format from USPTO at segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:11030.
                  Claim 1; SEQ ID NO 10066; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP05524 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US010836.
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29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VRTAÄEF 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200192523-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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WPI; 2003-721702/68.
N-PSDB; ADF76714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
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Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF76715;
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                                                                                                                                      The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1)

in the specification). ABN15762 to ABN2752 encode the human ORFX

proteins given in ABP0010 to ABP11500. ORFX proteins are useful for

treating or preventing a pathology associated with an ORFX-associated

disorder in humans, and in the manufacture of a medicament for treating a

cyndrome associated with ORFX-associated disorder. ORFX polymucleotide

sequences can be used in gene therapy. ORFX sequences can be used in the

treatment of cancer, hyperproliferative disorders, intrhosis of liver,

psociasis, benign tummours, keloid, degenerative disorders, haemorrhage,

costeoarthritis, neurodegenerative disorders, disorders related to organ

transplantation, cardiovascular diseases, diabetes mellitus, systemic

lupus erythematosus, hypertrension, hypothyroidism, cholesterol ester

ctransplantation, cardiovascular diseases, diabetes mellitus, systemic

lupus erythematosus, hypertension, hypothyroidism, cholesterol ester

ctransplantation cardiomanne deficiencies and disorders, infectious

diseases, autoimmune disorders such as multiple sclerosis, rheumatorid

atthritis, autoimmune inflammatory eye disease. ORFX proteins are also

conseful for treating burns, incisions, ulcers, for treating osteoporosis,

conseful for treating burns, incisions, ulcers, for treating osteoporosis,

consection or regeneration and treatment of lung or liver fibrosis,

contection or regeneration and treatment of lung or liver fibrosis,

contection or regeneration and treatment of lung or liver fibrosis,

creperfued amange. N.B. The sequence data for this patent did not

form part of the printed specification, but was obtained in electronic

form part of the brinted specification, but was obtained in electronic

contents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                              Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                               preventing and treating cardiovascular disease, neurodegenerative hyperproliferative disorders and autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%; Score 18; DB 5; Length 112; 42.9%; Pred. No. 1.4e+03; ive 1; Mismatches 3; Indels
                                                                                                              Disclosure; SEQ ID NO 11030; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB29900 standard; protein; 121 AA.
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20-JAN-2000; 2000US-0177050P.
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Matches 3; Conservative
WPI; 2002-106308/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 IATTAEF 65
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                  N-PSDB; ABN21276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB2990(
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The invention relates to the isolation of genes AAC63410-C63458 encoding the human secreted proteins AAB29802-B29850. This sequence represents a cragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to the protein. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, c.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal cract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's clisease, allergies, autoimmune haemolytic anaemia, autoimmune cristories, diabetes mellitus, Crohn's disease, multiple sclerosis, thematoid arthritis and ulcerative colitis; (c) cardiovascular disorders cuerebral anoxia and epilepsy; and (f) infectious diseases cuerebral anoxia and epilepsy; and (f) infectious diseases cuerebral anoxia and epilepsy; and (f) infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor-ligand interaction; cytostatic; chondrocyte; tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 3; Length 121; Pred. No. 1.5e+03; Indels 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein SeqID 390.
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                                                                                                                                                                                                                                                                            Disclosure; Page 479; 495pp; English.
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    Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunte B,
, Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003WO-US005241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark H, H
, Wood WI,
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Ruben SM,
                                                                          WPI; 2000-647424/62
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in the formation, differentiation and maintenance of multicellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

Corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

Corecived from other cells and the immediate environment. The information corrected properties (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or sequence is the amino acid sequence of a human PRO protein of the
                                                                                                                                                      This invention relates to novel nucleic acids encoding human PRO secreted
                  New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean partial protein phosphatase 2A regulatory subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 7; Length 137;
Pred. No. 1.7e+03;
0; Mismatches 3; Indels
                                                                                                                Claim 10; SEQ ID NO 390; 918pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY99815 standard; protein; 139 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VITAREF 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VXXXAEF 7
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                                                                            diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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The present sequence is soybean protein phosphatase 2A regulatory subunit B. The nucleotide sequence encoding this protein was identified in clone src2.pkO31.9 of a cDNA library made from soybean eight-day-old root infected with cyst nematode. BLAST analysis showed that the sequence encodes protein phosphatase 2A regulatory subunit B. The nucleotide sequence may be used for the recombinant production of the protein in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in fermentation culture. The protein may then be used to modulate the process of reversible protein phosphorylation in plants. It may be used directly to supplement a plant's own production of the enzyme or to rectify mutations that result in the expression of inactive protein. The protein may also be used to test for modulators of protein phosphorylation which may be used to alter the activity of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                 Polynucleotides encoding plant protein phosphatase useful for modulating reversible protein phosphorylation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel human secreted polypeptides. The oblypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 3; Length 139;
Pred. No. 1.8e+03;
0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                      Claim 12; Page 48-49; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU31774 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #2265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2001; 2001WO-US008656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
WPI; 2000-431599/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VITSAEF
                 N-PSDB; AAA48570
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU31774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 46
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Gaps

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Length 148, 3; Indels

Score 18; DB 5; | Pred. No. 1.9e+03; 0; Mismatches

Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative

69 VSTLAEF 1 VXXXAEF

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identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

AAU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55521). The nucleic acid sequence, is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent wor20177334 (published 18-0CT-2001) which is available in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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                                                                                                                                                                                                                                                                                                       Score 18; DB 4; Length 144;
Pred. No. 1.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renault P, Ehrlich SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID NO 2081; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB55379 standard; protein; 148 AA.
                                                                                                                                                                                                                               secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis protein yvaC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                        57.1%;
                                                                                                                                                                                                                                                                                                         81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                    VITAAEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
                                                                                                                                                                                                                                                                    Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001.
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16-MAY-2002
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16-MAR-2000; 2000WO-US006828.

19-MAR-1999;

WO200056767-A1. sapiens.

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28-SEP-2000

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinfammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.

Human secreted protein BLAST search protein SEQ ID NO: 141.

(first entry)

02-FEB-2001

AAB34523;

AAB34523 standard; protein; 155 AA.

RESULT 48 AAB34523

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The invention relates to the isolation of genes AAC59624-C59669 encoding the human secreted proteins AAB14439-B34484. This sequence represents a peptide fragment homologous to the protein encoded by the gene isolated in the present invention. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, and other cancers of the darenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders end other cancers of the alergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid architis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 373; 384pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing, treating or ameliorat
Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                    99US-0125358P.
99US-0169616P.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-602216/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA,
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standardise OS field)

Sequence 148 AA

format from USPTO at segdata.uspto.gov/seguence.html

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant the excombinant DNA construct and growing the transformed plant with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, collerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved lightin production or improved glad condition or production. This sequence represents a bacterial polypeptide used in the scope of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen X, Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 16932; 122pp; English.
                                                                                                                                                                                                                                                 ADS27899 standard; protein; 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial polypeptide #16932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEN X.
GOLDMAN B S.
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                                                                  44 VATLAEF 50
1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004
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                                                                                                                                                                                                                                                                                                                    ADS27899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SLAT/) (CHEN/) (GOLD/)
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(HINK/)
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ADS27899

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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by conserved. The disorders include SAPHO syndrome (Syndrome Gyndrome Gyndro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalmitis; bone; joint; central nervous system; ELLSA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang SS, Bhatia A; Jen S, Carter D;
                                                 Length 159;
                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #28527.
                                                 Score 18; DB 8;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 28826; 1069pp; English.
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                         AAU67631 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2001; 2001WO-US012865
                                                 81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-2002 (first entry)
                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes.
                                                                                                                                                                                                         142 VAAEAEF 148
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                                                 Query Match
Best Local Similarity
                                                                                                                                                     1 VXXXAEF
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Sequence 159 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             AAU67631;
                                                                                                    Matches
                                                                                                                                                                                                                                                                                   RESULT 50
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RESULT 51 ABM64150

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AAB28213 standard; protein; 169 AA.
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99US-00396313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-2000; 2000WO-US005431.
                                                                                                                                                      81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                               4; Conservative
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                                                                                                                                                                                                                                                                          100 VAVTAEF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                    Query Match
Best Local Similarity
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Matches 4; Conserv
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                                                                                                                   Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200052165-A2.
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17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                AAB28213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                   RESULT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynuclectide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (BMM35624-ABM64536) and to immunogenic fragments of by a canes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a collingual proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes invention; fusion proteins composition (comprising P. acnes polypeptides, polypeptide and an isolated T cell population comprising T cells prepared via this method, a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit con detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting or treating an immune response specific for a P. acnes for polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes for nucleic acid hybridisation. The vaccine composition is useful for theating acne under the kit is useful for performing a diagnostic assay. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carter D;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes predicted ORF-encoded polypeptide #28826.
                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                             Length 162;
                                                                         Score 18; DB 4; Length 162
Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 28826; 1481pp; English.
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                            ABM64150 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001US-00978825.
                                                                           81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                      Query Match
Best Local Similarity 57.1
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.
                                                                                                                                                                                             100 VAVTAEF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-381789/36
                                                                                                                                                        7
                                                                                                                                                      1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACF64533
                                      Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2003
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sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            new human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to immunogenic portions of new human breast tumour antigens (AAB28183-B28214) and their coding sequences (AAG69645-G26944). The breast tumour antigen polypeptides of the present invention and their coding sequences are useful for inhibiting the development of breast cancer in a patient. The breast tumour antigen polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for treating breast cancer, and for diagnosing and amonitoring the cancer. The present sequence is a immunogenic portion for one such human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast tumor antigen polypeptides and polynucleotides, useful for manufacturing vaccines and compositions for treating, diagnosing, and monitoring breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; vaccine; human; breast tumour; antigen; breast cancer.
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                                                                                                                                                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                Score 18; DB 6;
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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(first entry)

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Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                           Streptococcus polypeptide SEQ ID NO 8518.
                           ABP29671 standard; protein; 193 AA
                                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-00026333
                                                                                                                                                                                                                                                                                                                                     07-MAR-2001; 2001GB-00005640
                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                              Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-352536/38.
N-PSDB; ABN70302.
                                                                                                                                                                                                                        WO200234771-A2.
                                                                                                                                                                                                                                                                                                                       24-NOV-2000;
                                                                                 02-JUL-2002
                                                                                                                                                                                                                                                    02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
Tettelin H;
                                                       ABP29671;
 RESULT 54
              ABP2967
                                          ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel lactic acid bacteria (Lactobacillus rhamnosus strain HN001) polynucleotide sequences, and the proteins encoded by them. Also disclosed are oligonucleotide probes and primers, and genetic constructs comprising the polynucleotide sequences of the invention. The polynucleotide sequences are useful for preparing a vaccine against bacterial infections or for improving the properties of microbes used in the manufacture of milt-derived products, food products, food additives, nutritional supplements, bloactive substances or probiotic supplements, and for modifying the flavour, around texture and/or nutritional value of foods. They are also useful for identifying microorganisms having a trait associated with the polynucleotide. The present sequence represents a novel L. rhamnosus polynucleotide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence or or properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide from Lactobacillus rhamnosus HN001 strain, useful for preparing a vaccine against bacterial infections or for modifying the flavor, aroma or nutritional benefits of a bioactive or probiotic supplement product.
                                                                                                                                    Lactic acid bacteria; vaccine; bacterial infection; microbe; milk-derived product; food additive; mutritional supplement; bloactive substance; problotic supplement; flavour; aroma; texture; nutritional value; food; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 179;
                                                                                                           Lactobacillus rhamnosus polypeptide sequence #78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 8; I
Pred. No. 2.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glenn M, Havukkala IJ, Lubbers M, Dekker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; SEQ ID NO 199; 54pp; English.
                                                                                                                                                                                                                        Lactobacillus rhamnosus; strain HN001.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
                           ADI67204 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                     99US-0147852P.
99US-0147853P.
99US-0152031P.
                                                                                                                                                                                                                                                                                                                                                                             01-SEP-1999; 99US-0152032P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2001; 2001US-00971536.
                                                                                                                                                                                                                                                                                                          03-OCT-2002; 2002US-00264213
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-090459/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADI67079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 179 AA;
                                                                                                                                                                                                                                                    US2004009490-A1.
                                                                                                                                                                                             antibacterial.
                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1999;
01-SEP-1999;
                                                                                 22-APR-2004
                                                                                                                                                                                                                                                                                                                                       09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                    09-AUG-1999;
                                                                                                                                                                                                                                                                                15-JAN-2004
                                                     ADI67204;
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RESULT 5
ADI67204
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Fraser C;

Masignani V, Margarit Y RosI, Grandi G,

2000GB-00028727

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 548 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a streptococcus ample (1) is are used to detect Streptococcus in a composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chomatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.5e+03;
0; Mismatches 3; Indels
                                                                                                                                                                        Claim 1; Page 3962; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 81.8%;
Similarity 57.1%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193 AA;
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VTSIAEF 47

41

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Gaps

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3; Indels

Local Similarity 57.1 les 4; Conservative

Matches

162 VSTIAEF 168

1 VXXXAEF

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RESULT 55

09730329-59ed.rag

**ABP25742** 

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PAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY348912. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                  Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 2; Length 204; Pred. No. 2.7e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson MA, Agius CT,
                                                                                                            Porphorymonas gingivalis protein PG64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO66356 standard; protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 524; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              98AU-00001546.
98AU-00002264.
98AU-00002911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98AU-00003128.
98AU-00003338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98AU-00003654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98AU-00004963.
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57.1%;
                                                                                                                                                                                                                                                                                                                       98WO-AU001023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98AU-00004917
                                                                          (first entry)
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                                                                                                                                                                                                           Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                       revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barr IG, Pa
I, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-385613/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VXXXAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX91751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CSTC-) CSL LTD
                                                                                                                                                                                                                                            WO9929870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1998;
30-JUL-1998;
04-AUG-1998;
                                                                                                                                                                                                                                                                                                                       10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1998;
22-MAY-1998;
                                                   20-MAR-2003
25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hocking DM,
                                   27-AUG-2003
                                                                                                                                                                                                                                                                                    17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998
09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1998
                                                                                                                                                                     antigenic.
AAY34533;
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ABO66356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus handle (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                               Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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Pred. No. 2.6e+03;
0; Mismatches 3; Indels
                                                                                                                              Streptococcus polypeptide SEQ ID NO 660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 3219; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY34533 standard; protein; 204 AA.
             ABP25742 standard; protein; 197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001WO-GB004789
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V,
                                                                                                                                                                                                                                              Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-352536/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 197 AA;
                                                                                                                                                                                                                                                                                40200234771-A2.
                                                                                        02-JUL-2002
                                                                                                                                                                                                                                                                                                                     02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Felford J,
                                                 ABP25742;
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Margetts MB;

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Gaps

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RESULT 56 AAY34533 ID AAY3 XX

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Margetts MB;

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Porphorymonas gingivals (PO) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the scolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                    Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection.
                                                                                                                                                                                                                                                                                                                                   AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 2; Length 221;
Pred. No. 2.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                 Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lonetto MA,
                                                                                                                                                                 Agius CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY85820 standard; protein; 225 AA.
                                                                                                                                                                  Patterson MA,
                                                                                                                                                                                                                                                                                                      Claim 1; Page 371; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. pneumoniae derived protein #29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
               98AU-00003128.
98AU-00003338.
98AU-00003654.
                                                               98AU-00004917.
98AU-00004963.
98AU-00005028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0024022P
98AU-00002911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hodgson JE,
                                                                                                                                                                    Barr IG, Pa
1, Webb EA;
                                                                                                                                                                                                                  WPI; 1999-385613/32.
N-PSDB; AAX91618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-159452/14.
N-PSDB; AAZ96199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGAAAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 221 AA;
                                                                                                                                   (CSFC-) CSF FLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9806734-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2000
                 23-APR-1998;
05-MAY-1998;
                                                                29-JUL-1998;
                                                                                                  04-AUG-1998;
                                                                                                                                                                                    Hocking DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY85820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY85820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                 Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 7; Length 214; 57.1%; Pred. No. 2.8e+03; ive 0; Mismatches 3; Indels
 Klebsiella pneumoniae polypeptide segid 12873
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 12873; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphorymonas gingivalis protein PG64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34400 standard; protein; 221 AA.
                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-00000839.
97AU-00001182.
98AU-00001546.
98AU-00002264.
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                                                                                                                                                                                                                     99US-0117747P
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis
                                                                                                                                                                                                                                                                                        Osborne M;
                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVSTAEF 192
                                                                                                                                                                                                                                                                                                                       WPI; 2003-895346/82.
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                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACH99907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
                                                                                                                     US6610836-B1
                                                                                                                                                                                                                     29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9929870-A1
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                                                                                                                                                    26-AUG-2003
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20-MAR-2003
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                                                                                                                                                                                                                                                                                        Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigenic
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Matches

RESULT 58 AAY34400

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R R R R X X P X X R X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B

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Gaps

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                                                        This invention describes novel isolated Streptococcus pneumoniae polymucleotides (see AAZ96173-206494) and their encoded proteins (see AAX95792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to expression or activity of interact with and inhibit or activate such a polypeptide. The polypeptides for DNA encoding them, via agene therapy) are also useful for inhibit such bacterial polypeptides. The polypeptides are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
Streptococcus pneumoniae proteins and related DNA - useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                        Score 18; DB 2; Length 225;
Pred. No. 3e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 24570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EW.
                                    Claim 5; Page 338-339; 640pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
             compounds for antibacterial activity
                                                                                                                                                                                                                                                                                                                                                                                                                ABB65926 standard; protein; 225 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                         81.8%;
57.1%;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1.,
Best A; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                    VMSAAEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                  Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; transgenic; enhanced seed oil; vegetable oil.
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Similarity 57.1%; Pred. No. 3e+03;
4; Conservative 0; Mismatches
                                                                                                                                                                                              Score 18; DB 4; Length 225. Pred. No. 3e+03;
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                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oil-associated gene related protein #1093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                                                              81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2003; 2003US-00389566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ravanello M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAURIE C C.
RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-142683/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                             7 VITABEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROGERS J A.
                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                             1 VXXXAEF
                                                                                                                                                   Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004025202-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oil-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laurie CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ49593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RAVA/)
(SAVA/)
(LEDE/)
(ROGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAUR/)
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ49593
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The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to serine protease HtrA. The protein, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean, protein phosphatase 2A; protein phosphorylation modulation, transgenic plant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acids from Streptococcus pneumoniae - useful, for identifying anti-bacterial(s) for treatment and prevention of
                                                                 coding region; ORF; open reading frame; antibacterial; infection; prevention; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean partial protein phosphatase 2A regulatory subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 2; Length 231;
Pred. No. 3.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Black MT, Hodgson JE, Knowles DJC, Lonetto MA,
                     Streptococcus pneumoniae encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY99822 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 85; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                              97WO-US019226.
                                                                                                                                                                                                                                                                                                                         96US-0029930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                         Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-286586/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV37380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200036121-A2
                                                                                                                                                                                                                                                                              27-OCT-1997;
                                                                                                                                                                                                                                                                                                                            01-NOV-1996;
                                                                                                                                                                                  WO9819689-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reid RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY99822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY99822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing wegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                               oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 8; Length 228;
Pred. No. 3e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ledeaux JR,
                                                                                                                                                                                                                                                                                                      Oil-associated gene related protein #1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 1581; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Savage T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW60988 standard; protein; 231 AA.
                                                                                                                                                          ADJ49577 standard; protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2003; 2003US-00389566.
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laurie CC, Ravanello M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAVA/) SAVAGE T.
(LEDE/) LEDEAUX J R
(ROGE/) ROGERS J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-142683/14
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                                           41 VEAAAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAURIE C C.
VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004025202-A1
                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60988;
                                                                                                                                                                                                          ADJ49577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 63
                                                                                                                                    ADD 49577

ADD 49577

ADD 49577

ADD 49577

ADD 60-01

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Gaps

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AAG27923 standard; protein; 239 AA.
                                             Example 2; Fig 8; 48pp; English
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99US-012318OP.
99US-0125788P.
99US-0126764P.
99US-0126764P.
99US-0126764P.
99US-0128734P.
99US-0128734P.
99US-0128734P.
99US-013873P.
99US-013873P.
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99US-0134256P.
99US-0134218P.
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                        167 VTTVAEF 173
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                   1 VXXXAEF 7
                                                                                                                                                              therapeutic agents
                                                                                                                                                                                   Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                            17-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1999
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                                                                                                                                                                                                                                                                                                                                                     AAG27923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-
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                                                                                                                                                                                                                                                                                                          RESULT 66
                                                                                                                                                                                                                                                                                                                      AAG27923
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                                                                                                                                                                                                              B. The nucleotide sequence encoding this protein was identified in clone src2c.pk023.19;fis of a cDNA library made from soybean eight-day-old root infected with cyst nematode. BLAST analysis showed that the sequence encodes protein phosphatase 2A regulatory subunit B. The nucleotide sequence may be used for the recombinant production of the protein in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in fermentation culture. The protein may then be used to modulate the process of reversible protein phosphorylation in plants. It may be used directly to supplement a plant's own production of the enzyme or to rectify mutations that result in the expression of inactive protein. The protein may also be used to test for modulatores of protein phosphorylation mayino phosphorylation may also be used to test for modulatores of protein phosphorylation which may also used to alter the activity of the enzyme
                                                                                                                                                                                                      The present sequence is soybean protein phosphatase 2A regulatory subunit
                                                                                                                                                Polynucleotides encoding plant protein phosphatase useful for modulating reversible protein phosphorylation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease; HtrA; protein removal; periplasm; virulence factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones HC, Liu C, Hultgren SJ, Hruby DE, Franke CA, Evans AK;
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                                                                                         Rafalski JA, Klein TM;
                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 3; Length 236; 57.1%; Pred. No. 3.1e+03; ive 0; Mismatches 3; Indels
                                                                                         Lee J,
                                                                (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB61537 standard; protein; 236 AA.
                                                                                                                                                                                 Claim 12; Page 62; 73pp; English
                                                                                         Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SIGA-) SIGA TECHNOLOGIES INC (UNIW ) UNIV WASHINGTON.
                      99WO-US029823
                                            98US-0112541P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-2000; 2000WO-US017835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0140990P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                         Famodu OO, Miao G,
                                                                                                               WPI; 2000-431599/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-123028/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VITSAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalytic domain.
                                                                                                                           N-PSDB; AAA48577
                                                                                                                                                                                                                                                                                                                                                               Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200101147-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DegP protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-1999;
                     15-DEC-1999;
                                            16-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-2001
22-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                       The DegP (HtrA) protease (the present sequence) is a multifunctional protein essential for the removal of misfolded and aggregated proteins in the periplasm. DegP is essential for virulence in several Gram negative pathogens. The present invention relates to an assay for identifying inhibitors of DegP. The assay comprises mixing suspected DegP inhibitors whith DegP and a suitable substrate, preferably the major is pilm subunit of Pap pilus, and detecting changes in DegP activity. The compounds identified as inhibitors of DegP protease function are useful as
Assay for DegP protease inhibitors useful as therapeutic agents, involves mixing inhibitor of DegP activity with DegP and major pilin subunit of Pap pilus as substrate and detecting changes in DegP activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Matches

RESULT 67 AAR9719

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The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulates. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectionity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29329-AAU293379 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bscherichia coli, major nitroreductase protein, NfsA, Vibrio harveyi, NADH oxidoreductase Frp; flavin reductase P; enzyme; antibacterial; antituberculostatic, vulnezary; antiinflammatory; virucide; auditory; antitussive; litholytic; nephrotropic; gastrointestinal; antiulcer; bacterial growth inhibitor; bacterial infection; microbial infection; tuberculosis; respiratory infection; pronchitis; sinuatis; pneumonia; sore throat; diphtheria; acute epiglottitis; influenza; ottis media; bronchopneumonia; Legionnaire's disease; whooping cough; urethritis; cystitis; pyelonephritis; colitis; enteritis; gastric ulcer; cholera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.
                                                                                                      mar regulated polypeptide; NIMR; microbial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major nitroreductase protein NfsA amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 4; Length 240; 57.1%; Pred. No. 3.2e+03; ive 0; Mismatches 3; Indels
                                                                    Novel mar regulated protein (NIMR) #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 526; 526pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP57429 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                   Alekshun MN;
                                                                                                                                                                                                                                                         08-MAR-2001; 2001WO-US007478.
                                                                                                                                                                                                                                                                                             10-MAR-2000; 2000US-0188362P
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                                  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                     Barbosa TM,
                                                                                                                                                                                                                                                                                                                                 (TUFT ) TUFTS COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 VAQAAEF 76
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                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602769,
N-PSDB; AAS46278
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                                                                                                                                                                                WO200170776-A2.
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AAU29379;
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Matches
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ABP57429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of the nitroreductase enzyme ncoded by the E.coli nfsA gene. The gene was isolated as given in Kumar and Jayaraman, (1991) J.Bioscence, 16, 145-159, and was subcloned to produc the plasmid pAJ102. The gene can be used to generate strains of E.coli which are senstive to mutagenic and carcinogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli nitro:reductase gene - useful to produce mutagen or carcinogen sensitive strain, using E. coli host.
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli; nfsA; nitroreductase; mutagen; carcinogen.
                                                                                                                                                                                                   Score 18; DB 3; I
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU29379 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         AAR97195 standard; protein; 240 AA.
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               99US-0161405P
99US-0161359P
99US-0161359P
99US-0161360P
99US-0161361P
99US-0161922P
99US-0161932P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.coli nitroreductase protein.
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57.1%;
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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               25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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RESULT 68 AAU29379 ID AAU29 XX

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AAY34534;
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    g
                                                                                                                                                                                                                                                                                                                                                        the erroryclic compounds (I) or their salts. (I) has antibacterial, antituberculostatic, vulnerary, antiinflammatory, virucide, auditory, antituberculostatic, vulnerary, antiinflammatory, virucide, auditory, contituberculostatic, nephrotropic, gastrointestinal and antiulcer activities, and can be used as abacterial growth inhibitor. (I) can be used for treating bacterial or microbial infection and tuberculosis in commans as well as animals. (I) can also be used as sterilisants, antiseptics, adjuvants in wound dressings (e.g. bandages) and adjuvants in wound cleaning methods (e.g. swipes or gavage); for treating upper and lower respiratory tract infections (e.g. bronchitis, sinusitis, core throat, chronic streptococcal infections diphtheria, acute epiglotticis, influenza, chronic bronchitis, middle ear infections (critis media) bronchopneumonia, regionnaire's disease, atypical pneumonia or whooping cough), urinary tract infections (e.g. urethritis, cystitis, pyelonephritis (kidney infection), asymptomatic bacteuria, infections, colitis, acute urethral syndrome or recurrent urinary tract infections, gastrointestinal infections, chocars, duodenal ulcers, borne infections, colitis, entertisis, gastric ulcers, duodenal ulcers, cused for inhibiting bacterial growth in a non-living system. The present squence represents an E. coli major nitroreductase protein Nfsh which is example fication of the present inversent bacterial bacterial bacterial paretrial protein bacterial promiten and actis sequence from the luminescent bacterium vibrio harveyi in the example fication of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                               nitrofuran containing heterocyclic compounds useful in treating e.g.
                                                                                                                                                                                                           Clement JJ;
                                                                                                                                                                                                                                                                                                                                                   present invention describes nitrofuran compounds substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli, major nitroreductase protein; NEBA; Vibrio harveyi, NADH oxidoreductase Frp; flavin reductase P; enzyme; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 3.2e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention
duodenal ulcer; pancreatitis; typhus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP57430 standard; protein; 240 AA.
                                                                                                                                                                   (ESSE-) ESSENTIAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 23; 50pp; English
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                                                                                                            25-JUN-2002; 2002WO-US020387.
                                                                                                                                         25-JUN-2001; 2001US-0300636P.
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57.1%;
                                                                                                                                                                                                             Magee AS, Roy A, Moe ST,
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Best Local Similarity 5/...
4; Conservative
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                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 240 AA;
                                                      WO2003000255-A1.
                                                                                                                                                                                                                                                                                              tuberculosis
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The present invention (1) to their sails. (1) has antibacterial, antituberculostatic, vulnerary, antinflammatory, virucide, auditory, antituberculostatic, vulnerary, antinflammatory, virucide, auditory, antituberculostatic, nephrotropic, gastrointestinal and antiulcer activities, and can be used as a bacterial growth inhibitor. (1) can be used for treating bacterial or microbial infection and tuberculosis in humans as well as animals. (1) can also be used as sterilisants, and adjuvants in wound dressings (e.g. bandages) and adjuvants in wound cleaning methods (e.g. swipes or gavage); for treating upper and lower respiratory tract infections (e.g. bronchitis, sinusitis, preumonia, sore throat, chronic streptococcal infections, diphtheria, acute epiglottitis, influence, chronic bronchitis, middle ear infections of otitis media), bronchopneumonia, Legionnaire's disease, atypical pneumonia or whooping cough, urinary tract infections (e.g. urethritis, cystitis, pyelonephritis (kidney infection), asymptomatic bacteria, infections, contitis, acute urethral syndrome or recurrent urinary tract infections), gastrointestinal infections of bacterial origin (e.g. food borne infections, colitis, enteritis, gastrointestinal growth in a non-living system. The present sequence represente a NADH oxidoreductase FTP (flavin reductase P) amino acid sequence represente a NADH oxidoreductase FTP (flavin reductase P) amino acid sequence from the luminescent bacterium Vibrio harveyi which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nitrofuran containing heterocyclic compounds useful in treating e.g
antitussive; litholytic; nephrotropic; gastroinfestinal; antiulcer; bacterial growth inhibitor; bacterial infection; microbial infection; tuberculosis; respiratory infection; bronchitis; sinusitis; pneumonia; sore throat; diphtheria; acute epiglottitis; influenza; otitis media; bronchoneumonia; legionnaize de disease; whooping cough; urethritis; cystitis; pyelonephritis; colitis; enteritis; gastric ulcer; cholera; duodenal ulcer; pancreatitis; typhus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clement JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes nitrofuran compounds substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 3.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ali J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Griffith JP, Ala PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ESSE-) ESSENTIAL THERAPEUTICS INC. (PLIV ) PLIVA DD ZAGREB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY34534 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 23; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-2002; 2002WO-US020387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-2001; 2001US-0300636P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Magee AS, Roy A, Moe ST,
Navia M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-201374/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003000255-A1.
                                                                                                                                                                                                                                                                                                                                           Vibrio harveyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, bustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies contacting the capression and activity of P. acnes polypeptides and cherefore treat P. acnes proteins. These antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by curryen linked immunosorbent assay (ELISA). Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes predicted ORF-encoded polypeptide #28230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 4; Length 247; 57.1%; Pred. No. 3.3e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Wang SS,
', Jen S, Carter D;
                                                                                  dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 28230; 1069pp; English.
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                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                   20-APR-2001; 2001WO-US012865.
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e J, Zhang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                           Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS59774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 247 AA;
                                                                                                                                                                WO200181581-A2.
                                                                                                                                                                                                         01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34363. AAX91802 to AAX91999 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                          Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson MA, Agius CT, Rothel LJ, Margetts MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
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                                                                                                   Porphorymonas gingivalis protein PG65.
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98AU-00003654.
98AU-00004917.
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98AU-00002911.
98AU-00003128.
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               (revised)
(revised)
(first entry)
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                                                                                                                                                                                                       Porphyromonas gingivalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ross BC, Barr IG, Pa
Hocking DM, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-385613/32
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               27-AUG-2003
20-MAR-2003
25-AUG-1999
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23-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1997
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10-MAR-1998
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                                                                                                                                                                  antigenic.
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Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
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                                                                                              Porphorymonas gingivalis protein PG65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 372; 588pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98AU-00003654.
98AU-00004917.
98AU-00004963.
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98AU-00001546.
98AU-00002264.
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57.1%;
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98AU-00003338
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                                                       (first entry)
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                                                                                                                                                                                               Porphyromonas gingivalis
                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385613/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CSLC-) CSL LTD.
                                                                                                                                                                                                                                    WO9929870-A1.
                27-AUG-2003
20-MAR-2003
25-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1998
                                                                                                                                                        antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB69168
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding a Propionizacterium acrass protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acraes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a ddittionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; polypeptide of the invention; and the invention; and immune response specific for a P. acraes in the invention and proteins comprising proteins comprising a polypeptide of the invention; at this method; a vaccine composition (comprising P. acraes polypeptides, polymetedetides, antibodies, fusion proteins, T cell populations, or attigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acraes in a patient; and a method for inhibiting the development of P. acraes in a patient; The P. acraes polypeptides, polymetectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for antigen-presenting cells that express the polypeptides are useful for adiagosing, preventing or treating acrae polypeptides are useful for diagnosing, preventing or treating acrae protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulating an immune response against P. acraes, or for treating acrae and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acraes polymelection, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                  Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                              Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 6; I
Pred. No. 3.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 28230; 1481pp; English.
                                   immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                              Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                               Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                           11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
57.1%;
                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                              Skeiky YAW,
ng S, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 57.1.
4; Conservative
                                                                          Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-381789/36.
N-PSDB; ACF64703.
                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 VAVTAÈF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 247 AA;
                                                                                                               WO2003033515-A1
                                                                                                                                                                                                                                                                                                              Mitcham JL,
                                                                                                                                                      24-APR-2003
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Margetts MB;

Agius CT, Rothel LJ,

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ö
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX34883. AAX91802 to AAX91898 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                  Length 248;
                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 2; Length 248
Pred. No. 3.3e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 34296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
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AAY34401 standard; protein; 248 AA

RESULT 74 AAY34401 ID AAY: XX AC AAY:

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AAY34401

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07-AUG-2003; 2003US-0492997P.
10-NOV-2003; 2003US-0518286P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0117747P
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                      Mcalpine JB,
                                                                          WPI; 2004-593481/57.
N-PSDB; ADR01210, ADR01256.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osborne M;
                                                                                                                                                                                                                                                                                                                                                123 VAVAAEF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-895346/82.
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                                                                                                                                                                                                                                         dibenzodiazepinone
                                                                                                                                                                                                                                                                                                                            1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACH97479
                                                                                                                                                                                                                                                              Sequence 253 AA;
                                                      Bachmann BO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6610836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                           AB063928;
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 77
                                                                                                                                                                                                                                                                                                                                                                                              AB06392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA dequences (ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic, Antibacterial, Antiinflammatory;
Cancer cell growth inhibitor; Lipooxygenase inhibitor;
farnesyl dibenzodiazepinone; cancer; bacterial infections; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.
                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farnesyl dibenzodiazepinone biosynthetic ORF23 protein HYDK, SEQ ID
          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 34296; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 18; DB 4; Length 249; 42.9%; Pred. No. 3.3e+03; ive 1; Mismatches 3; Indels
                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micromonospora sp.; strain 046-EC011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR01255 standard; protein; 253 AA.
                                                                                                                                                                                   PWD,
                                                                                                          23-MAR-2001; 2001WO-US009231
                                                                                                                             23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2004; 2004WO-CA000069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2003; 2003US-0441126P
                                                                                                                                                                                                                                                                                                                                                                                                                                   Locary Match
Best Local Similarity 42.99,
Share 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                   굼
                                         Drosophila melanogaster.
                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                        2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
ISASAEF 53
                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
                                                                                                                                                                                                        WPI; 2001-656860
N-PSDB; ABL13271
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004065591-A1
                                                               WO200171042-A2
                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2004
                                                                                    27-SEP-2001.
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The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel farnesyl dibenzodiazepinone compounds can be obtained by cultivation of a novel strain of Micromonospora sp., i.e. 046-ECO11 or [S01]046. The compounds are excellent tumour growth inhibitors as well mammalian lipooxygenase inhibitors and so are useful for treating cancer, pre-cancerous conditions, bacterial infections and inflammation in mammal. The present sequence is a protein involved in the biosynthetic pathway for a farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                            Piraee M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 8; Length 252.
Pred. No. 3.4e+03;
                                                                            Farnet CM,
                                                                                                                                                                                                                                                        New farnesyl dibenzodiazepinone compounds useful for e.g. cancer, bacterial infections and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella pneumoniae polypeptide segid 10445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 10445; 932pp; English.
                                                                            Zazopoulos E,
                                                                                                                                                                                                                                                                                                                                                                       Claim 53; SEQ ID NO 46; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO63928 standard; protein; 255 AA.
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(ECOP-) ECOPIA BIOSCIENCES INC
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The TABLE CONTROLLED ATTIVE CONTROLLED ACCENTING STRUCTURE STATES THE CONTROLLED ACCENTING STATES AND THE CONTROLLED ACCENTING STATES AND ACCENT AND THE C. Glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of expression in host cells and production or modulation of production of carporterinogenic anno acid (preferred), a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, an aromatic compound, a vitamin, a cofactor, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) containing them are used for diagnosing the presence or activity of cortaining them are used to map genomes of organisms related to C. Glutamicum, identify and localise C. Glutamicum sequences of interest, in thurstion, in modulating SMP protein activity, in modulating the relation activity, in modulating the map denomes of cortaining the containing the modulating sMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP), NADPH)
                                                                                                  New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                         AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                              Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 4; Length 258; Pred. No. 3.5e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochiai K,
                                Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C glutamicum protein fragment SEQ ID NO: 5807.
                                                                                                                                                                           Claim 20; Page 1004-1005; 1246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizoguchi H, Ando S, Hayasl
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG92053 standard; protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00377484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2001 (first entry)
                                                                                                                                                 carbohydrates or enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic acid synthesis.
                                Pompejus M, Kroeger
                                                           WPI; 2001-061975/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VATGAEF
                                                                         N-PSDB: AAF71659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 258 AA;
   (BADI ) BASF AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG92053;
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AAG92053
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                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
regulatory element; and a cell comprising the recombinant expression vector. The nuclaic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                  Gaps
                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum SMP protein sequence SEQ ID NO:600.
                                                                                                   81.8%; Score 18; DB 7; Length 255; 57.1%; Pred. No. 3.4e+03;
                                                                                                                                3; Indels
                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                   AAB79542 standard; protein; 258 AA.
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99DE-01031424.
99DE-01031428.
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99DE-01042123.
99DE-01042125.
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99DE-01031413.
99DE-01031419.
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99US-0143208P.
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99DE-01031562.
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99DE-01031433
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                                                                                                                 57.1%;
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                4; Conservative
                                                                                                                                                                                           VAQAAEF 91
                                                                                                                                                            1 VXXXAEF 7
                                                                                                                 Best Local Similarity
                                                                         Sequence 255 AA;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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09-JUL-1999;
14-JUL-1999;
14-JUL-1999;
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-JUL-1999;
-JUL-1999;
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                                                                                                     Query Match
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21-MAR-2000 (first entry)
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Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
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N-PSDB; AAZS4505.
                                                                                                                                                                                                                                                                                                                                                                        39 VASNAEF 45
                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
N-PSDB; AAZ54506.
                                                                                                                                                                                                                                                                     Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9957280-A2.
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25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY75743;
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria and organic acide, vitamins, saccharides and organic acide, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence date for this patent electronic form part of the printed specification, but was obtained in electronic format directly from the European Patent Offlice
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                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
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Scalato E, Scarselli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis ORF 981 protein sequence SEQ ID NO:2960.
                                                                                                Claim 17; SEQ ID NO 5807; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                    / Match 81.8%; Score 18; DB 4; Length 258; Local Similarity 57.1%; Pred. No. 3.5e+03; nes 4; Conservative 0; Mismatches 3; Indels
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Ratti (
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Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY75744 standard; protein; 266 AA.
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98US-0094869P.
98US-0099062P.
98US-0103749P.
98US-0103794P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis
          2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                       1 VXXXAEF 7
          WPI; 2001-376931/
N-PSDB; AAH67272.
                                                                                                                                                                                                                                                                                             Sequence 258 AA;
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02-SEP-1998;
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09-OCT-1998
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                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                               Matches
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ5456 and AAZ54616 to AAZ5437 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
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Scalato E, Scarselli M;
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Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 3; Length 266;
Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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, Pizza M, Rappuoli R, Ratti G,
                                                                                                          Claim 2; Page 1384; 1453pp; English.
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98US-0098694P.
98US-0098624P.
98US-0103749P.
98US-0103744P.
98US-0103764P.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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AAZ5301S to AAZ54516, AAZ54577 to AAZ5461S, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54613 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisseria bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to acreen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols. (Updated on 12-SBP-2003 to standardise OS
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                                       Claim 2; Page 1383; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY95653 standard; protein; 268 AA.
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99GB-00000952.
99GB-00001948.
99GB-00002074.
99GB-00002078.
99GB-00002088.
99GB-00002879.
99GB-00002879.
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57.1%;
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     vaccines and diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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N-PSDB; AAA50077.
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Best Local Similarity
Matches 4; Conserv
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23-FEB-1999
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                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N gonorrheae polymucleotides and polypeptides: AAZ54577 to AAZ54576 and AAZ54616 to AAZ54713 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polymucleotides, antibodies and compositions of the invention can be used as vaccines, a diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polymucleotides of the invention may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
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Scalato E, Scarselli M;
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Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                        Page 1383; 1453pp; English.
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   Pizza M, Rappuoli R,
   Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY75742 standard; protein; 266 AA.
                                                                                                                                                                                                                                                                                                                   used in gene therapy protocols
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98US-0098994P.
98US-0099062P.
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98US-0103796P.
99US-0121528P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                   Sequence 266 AA;
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Tettelin H,
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02-SEP-1998;
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21-MAR-2000
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25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY75742;
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                                                        Claim 2;
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AAY7574
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Matches
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                                                 The present sequence is that of the protein product of the BASB071 gene (see AAA50077) of Neisseria meningitidis ATCC 13090. The protein contains aleader sequence, have sequence characteristic of a lipoprotein signal sequence, and aleader sequence, and shows significant similarity to the Weisseria gonorrhoeae His protein. The invention provides novel N. meningitidis BASB051, BASB057, BASB060, BASB061, BASB065, BASB066, BASB066, BASB067, POLYPEPTIGES (see AAY50670-77) encoding them. These polypeptides and polynucleotides are used to produce medicaments, especially vaccines, to generate immune responses in an animal (claimed). Antibodies directed against the polypeptides are used in the treatment of N. meningitidis disease (claimed). The polypeptides and polynucleotides can also be used as diagnostic reagents for the diagnosis or staging of N. meningitidis disease, and for the detection of an infectious organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a mandicament for treating or preventing a condition (e.g., meningatis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meningitis; virulence; gene; antibacterial; vaccine; veterinary; infection; Gram-negative bacteria; antimicrobial.
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU72995 standard; protein; 268 AA.
                   Claim 1; Page 110; 127pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    response to a drug
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                                                                                                                                                                                                                                                                                                                                         Sequence 268 AA;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid uncleic acid, (2) a host cell containing the vector; (3) an isolated or nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway identifying a gene required for cellular proliferation or the biological pathway in which a prolleration-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
the identification of an antimicrobial drug. The vaccines have prophylactic applications. AAU72911-AAU73014 represent N. meningitidis virulence proteins of the invention
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Xu HH;
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                                                                                                                Score 18; DB 5; Length 268;
Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #22690.
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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                                                                                                                      81.8%;
57.1%;
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Trawick JD,
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                                                                                                                    Query Match
Best Local Similarity
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                                                                                  Sequence 268 AA;
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Wall D,
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             product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. acruginosa. The present sequence is enroded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present of the printed specification, but was obtained flow, who, int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 6; Length 268; 57.1%; Pred. No. 3.6e+03;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #23623.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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 compound's activity; (11) a culture
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Trawick JD,
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                                                                                                                                                                                                                                                                                                Sequence 268 AA;
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25-OCT-2001;
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Wall D,
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polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids for this patent did not form part of the printed specification, but was obtained in alloration forms or proliferation are present agequence data for this patent of the printed specification, but was obtained in a loratory or some and an activity or the strains and antibular and an activity or the strains and antibular and an activity or activity and an activity and an activity and an activity and an activity and activi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 6; Length 268;
Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-058415/05.
N-PSDB; ABZ40980.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200279243-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           awla NK, Khare R;
Baughn MR, Gietzen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human kinase and phosphatase protein designated KPP-16. Human KPP sequences have cytostatic, anticonvulsant, nootropic, neuroprotective, creebroprotective, anticonvulsant, nootropic, antiinflammatory and thyromimetic activities, and can be used in gene therapy. The human KPP polypeptides and polypuckes of the invention are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of KPP, such as cell
         comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Murage J, Swarnakar A, Chawla NK, Khare R; K, Ramkumar J, Gururajan R, Baughn MR, Gietza Wang JT, Favero KD, Becha SD, Richardson TW; Yue H, Lee EA, Marquis JP;
 antibodies that specifically bind to the proteins. The composition
                                                                                                                                                                                                      ö
                                                                                                                                                                Score 18; DB 6; Length 269;
Pred. No. 3.6e+03;
                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression e.g. cancer, AIDS, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; kinase; phosphatase; enzyme; KPP; cytostatic;
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 16; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hafalia AJA, Lee S, Murage J, Sw
Elliott VS, Tran UK, Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                      ADN61450 standard; protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human KPP-16 protein SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2002; 2002US-0426713P.
26-NOV-2002; 2002US-0429766P.
11-FEB-2003; 2003US-0447043P.
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                                                                                                                                                                  81.8%;
                                                                                                                                                                               57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                      4; Conservative
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Jin P, Hawkins PR,
                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                        1 VXXXAEF 7
                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                               Sequence 269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                          ADN61450;
                                                                                                                                                                                                                                                                            42
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                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response; immunotherapeutic agent; insulin dependent diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
proliferative (e.g. cancer, atherosclerosis), neurological (e.g. ADDS, epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. ADDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of KPP. The KPP sequences or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Administration of neglected target tissue antigens to modulate immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequences AAY57063-Y57091 are examples of neglected target
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 8; Length 269;
Pred. No. 3.6e+03;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calbindin 2 (Caletinin) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uveoretinitis; inflammatory response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57069 standard; protein; 271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tian J, Olcott A;
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                                                                                                                                                                                                                                                                                                                                                                               81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                         Sequence 269 AA;
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                                                                                                                                                                                                                                                                    polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57069;
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 determinants used as agents promoting tolerance agents have failed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomollatory; cancer; leukaemia; nervous system disorder; arthritis; inflammatton.
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Wang ZW;
                                                                                                                                        Gaps
                to induce an effective regulatory T cell response. NTTAS as agents promoting tolerance are anticipated to be safer than use of target
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J, Zhang J, Ren F, Chen R,
Goodrich R;
                                                                                                       81.8%; Score 18; DB 3; Length 271; 57.1%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                              AAM78464 standard; protein; 271 AA.
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Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                        Human protein SEQ ID NO 1126.
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
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15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                       4; Conservative
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                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                    1 VXXXAEF
                                                                           Sequence 271 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157190-A2
                                              determinants
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                                                                                                                                                                                                                                                                                                           AAM78464;
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Ma Y, Zh
Xue AJ,
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target
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The present invention describes a method (M1) for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. M1 involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesothelioma (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, and for determining prognosis or outcome of a cancer patient. The ratio of expression levels of differentially expressed genes is used as an indicator of cancer type, cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; malignant pleural mesothelioma; MPM; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
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                                                                                         Length 271;
                                                                                         Score 18; DB 4; Length 271
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                 sequence listing were missing at the time of publication
(AAK52582) and 3666 (AAM80020) are omitted as the
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                                                                                                                                                                                                                                                                                                                                                                                                                Calretinin (calbindin 2) SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                 ADB70324 standard; protein; 271 AA.
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                                                                                       h 81.8%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                      VGSSAEF 112
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                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                               1 VXXXAEF 7
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                                                      Sequence 271 AA;
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                                                                                                                                                                                                      901
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                                                                                                                                                                                                                                                           RESULT 91
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Sequence 271 AA;

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also calaimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the expression, a method for identifying a compound useful in treating a pecification, a method for identifying a compound the polypeptides given in the specification, a method for identifying a compound the polypeptides given in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                          Gaps
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Score 18; DB 7; Length 271;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE63979 standard; protein; 271 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
               81.8%;
57.1%;
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           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                         106 VGSSAEF 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woolf C, D'urso D,
                                                                                                                                                              1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003016475-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE63979;
                                                                                                                                                                                                                                                                                                                                                        RESULT 92

ADE63379

ADE63379

ADE63379

AND ADE63379

AND ADE6

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, and erivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence witch is differentially regulated in an animal subjected to pain and a true to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating the polypeptides or their antibodies. The polymocleotide or the compound that modulates its activity is useful for preparing a medicament for treating
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specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                        ..
                                                                                            Score 18; DB 7; Length 271;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human Protein P22676, SEQ ID NO 9929.
                                                                                                                                                                                                                                                                                                                ADE63983 standard; protein; 271 AA.
                                                                                                  81.8%; Sco
57.1%; Pre
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                Ouery Match
Best Local Similarity 57.12
Local 4; Conservative
                                                                                                                                                                                                                  106 VGSSAEF 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D'urso D,
                                                                                                                                                                              1 VXXXAEF 7
                                                            Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK; P22676.
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                                                                                                                                                                                                                                                                                                                                                        ADE63983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                            RESULT 93
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a first to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the
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pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pain; neuronal tissue; gene therapy, spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                              Length 271;
                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                              Score 18; DB 7; I
Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                          ADE63977 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein P47728, SEQ ID NO 9923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(FARB ) BAYER AG.
                                                                                                                                                                          Query Match
Best Local Similarity 57...
4; Conservative
                                                                                                                                                                                                                                                                                                              106 VGSSAEF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-268312/26
                                                                                                                                                                                                                                                                        1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                        Sequence 271 AA;
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specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal the expression of a polynucleotide sequence which is differentially expressed in a mimal subjected to pain, a method for identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                      Score 18; DB 7; Length 271; Pred. No. 3.7e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Costigan M;
                                                                                                                                                                                                          frp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE63981 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Protein P47728, SEQ ID NO 9927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 1017pp; English.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                      81.8%;
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus.
                                                                                                                                                                                                                                                  Sequence 271 AA;
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polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the saquence presented is a rat protein (shown in Table 2 of the sequence data for this patent and not form part of the printed specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, determining prognosis or outcome of a cancer patient, selecting a course of treatment for a subject having or suspected of having malignant pleural mesothelioma (MPM) and evaluating treatment of MPM comprising determining the ratio of the expression level of a set of genes differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, malignant pleural mesothelioma, MPM; tumour, lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma, ovarian cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing the presence of cancer or non-cancer cells in tissue sample,
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 7; Length 271; S7.1%; Pred. No. 3.7e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human malignant pleural mesothelioma (MPM) protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gullans SR, Bueno R;
                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ37103 standard; protein; 271 AA
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                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-141744/14.
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                                                                                                                                                                                                                                                                                                                       Sequence 271 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
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squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer. The method is useful for diagnosing MPM in a subject suspected of having MPM which involves obtaining a tissue sample suspected of being cancerous from a subject and determining the expression of nucleic acid markers or its expression products in the tissue sample. This sequence represents a human MPM protein of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                         Gaps
cancer tissue. The cancer is chosen from MPM, lung adenocarcinoma,
                                                                                                                                                                                         ö
                                                                                                                                                              Score 18; DB 8; Length 271; Pred. No. 3.7e+03; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 32948.
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                         AAG27922 standard; protein; 284 AA
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9905-0123348P-
9905-0126284P-
9905-0126785P-
9905-0126785P-
9905-0128714P-
9905-0128714P-
9905-0138714P-
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99US-0132407P.
99US-0132484P.
99US-0132485P.
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99US-0134768P.
99US-0134941P.
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                                                                                                                                                                81.8%;
57.1%;
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                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                            106 VGSSAEF 112
                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                  1 VXXXAEF
                                                                                                                                         Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2,
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16-APR-1999;
19-APR-1999;
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30-APR-1999;
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23-APR-1999
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19-MAY-1999
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 8833333333338
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02-AUG-19 02-AUG-19 02-AUG-19 03-AUG-19 04-AUG-19 04-AUG-19 05-AUG-19 06-AUG-19 09-AUG-19	10-AUG-19 11-AUG-19 12-AUG-19 13-AUG-19 16-AUG-19 17-AUG-19 20-AUG-19 23-AUG-19 23-AUG-19 25-AUG-19 25-AUG-19 27-AUG-19	31 - AUG-19 01 - SEP-19 01 - SEP-19 10 - SEP-19 13 - SEP-19 15 - SEP-19 20 - SEP-19 24 - SEP-19 24 - SEP-19 25 - SEP-19 26 - OCT-19 06 - OCT-19 08 - OCT-19	12-0CT-19 13-0CT-19 13-0CT-19 13-0CT-19 14-0CT-19 14-0CT-19 14-0CT-19 14-0CT-19 12-0CT-19 21-0CT-19 21-0CT-19 22-0CT-19
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5124P. 5629P. 6621P. 67392P. 77222P. 7522P. 7522P. 8934P.	99999999999999999999999999999999999999	00000000000000000000000000000000000000	44325P. 444331P. 443334P. 443334P. 443334P. 4864334P. 6866P. 6866
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated oplypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                        Gaps
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                                                                                                  Score 18; DB 3; Length 284;
Pred. No. 3.9e+03;
                                                                                                                                       3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #29784.
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Yamamoto R,
                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                          ABU44257 standard; protein; 288 AA
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Carr GJ,
99US-016136IP.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                   57.1%;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                       Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans.
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N-PSDB; ACA48127.
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                                                                                                                       Best Local Similarity
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               28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Wall D,
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to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fite.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, avaccine composition (comprising P. acnes polypeptides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
product is overexpressed or underexpressed; (12) determining the extent
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Jones R, Carter D;
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Pred. No. 3.9e+03;
0; Mismatches 3; Indels
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Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 29488; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM64812 standard; protein; 290 AA.
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Vallieve-Douglass J;
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57.1%;
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ing S, Jen S,
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Best Local Similarity 57...
4; Conservative
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                                                                                                                                                                                                                                                                                     Sequence 288 AA;
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Barth B,
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ID ABM6
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9905-0139460P

9905-0139461P

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9905-0139462P

9905-0139463P

9905-013963P

9905-0139899P

9905-0140635P

9905-0140635P

9905-0140635P

9905-014205P

9905-014305P
             99US-0134219P
99US-0134721P
99US-0134721P
99US-0134941P
99US-0135224P
99US-0135229P
99US-0135229P
99US-013522P
99US-013522P
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99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-0137528P
99US-0137528P
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99US-0144334P.
99US-0144325P.
99US-0144632P.
99US-014484P.
99US-0145088P.
99US-0145088P.
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99US-014508P.
99US-014508P.
99US-014508P.
            14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
20-MAY-1999;
21-MAY-1999;
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10-JUN-15
10-JUN-15
14-JUN-15
16-JUN-19
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24-JUN-1
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04 - JUN- 1
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     contigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the completides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the catimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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161 4 US-09-270-767-43252 Sequence 432 169 4 US-09-248-7964-15773 Sequence 155 182 4 US-09-248-7964-15773 Sequence 443 185 1 US-07-741-940-6 Sequence 6, 185 1 US-08-289-548A-6 Sequence 6, 1 US-08-289-5486-6 Sequence 6, 1 US-08-452-658-6 Sequence 6,	7 77.3 185 1 US-08-452-655B-6 Sequence 6, 7 77.3 185 2 US-08-865-336-3 Sequence 3, 7 77.3 185 3 US-08-865-336-4 Sequence 4, 7 77.3 185 3 US-08-450-582-6 Sequence 6,	7 77.3 185 4 US-08-449-731-6 Sequence 6, Appl 77.3 187 1 US-07-956-700B-8 Sequence 8, Appl	777.3 187 1 US-08-476-537-8 Sequence 8, Appl 777.3 187 1 US-08-485-607-8 Sequence 8, Appl 777-7 103-08-18-18-18-18-18-18-18-18-18-18-18-18-18	7 77.3 187 3 US-09-43-943B-8 Sequence 8, Appl 7 77.3 187 3 US-09-433-043B-8 Sequence 8, Appl 7 77.3 187 4 US-09-248-796A-19854 Semuence 19854	7 77.3 189 3 US-08-779-764A-29 Sequence 7 77.3 189 4 US-09-563-456-29 Sequence	7 77.3 194 4 US-09-134-000C-3800 Sequence 7 77.3 199 4 US-09-328-352-6184 Sequence	7 77.3 206 4 US-09-270-767-58211 Sequence 7 77.3 210 1 US-07-741-940-4	7 77.3 210 1 US-08-289-548A-4 Sequence 7 77.3 210 1 US-08-452-654-4 Sequence	7 77.3 210 1 US-08-452-655B-4 Sequence 7 77.3 210 3 US-08-450-582-4 Sequence	7 77.3 210 4 US-08-449-731-4 Sequence	77.3 222 1 US-03-035-001A-0040 Sequence 7 77.3 222 1 US-07-056-700B-21 Sequence	7 77.3 222 1 US-08-485-607-21 Sequence Sequence 7 77.3 222 1 US-08-485-607-21 Sequence 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	77.3 222 3 US-09-4/3-0438-21 Sequence	77.3 230 4 US-09-107-532A-4412 Sequence 77.3 230 4 US-09-107-532A-4412 Sequence 77.7 21.11 116-00-124 000000000000000000000000000000000000	77.3 240 4 US-09-1034-000C-5009 Sequence 77.3 240 4 US-09-600C-5009 Sequence 77.3 240 4 US-09-600C-5000C-5009 Sequence 77.3 240 4 US-09-600C-5009 Sequence 77.3 240 4 US-09-600C-5000C-5009 Sequence 77.3 240 4 US-09-600C-5000C-5000C-5009 Sequence 77.3 240 4 US-09-600C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-5000C-500	77.3 248 4 US-09-2540-230-210/ Sequence 77.3 254 4 US-09-265-585C-126 Sequence 77.3 254 4 US-09-2740-267-38330	77.3 250 4 US-09-270-767-53537 Sequence 77.3 261 4 US-09-328-359-4725 Sequence	77.3 267 4 US-09-107-433-3575 Sequence	7 77.3 273 4 US-09-227-76-76-76-76-77-77-77-77-77-77-77-77-77	7 77.3 283 4 US-10-55-018E-4 Sequence	7 77.3 286 3 US-08-858-207A-331 Sequence	7 77.3 286 4 US-09-252-991A-18196 Sequence 7 77.3 287 4 US-09-583-110-4372 Sequence	7 77.3 290 4 US-09-902-540-10278 Sequence 7 77.3 302 4 US-09-543-681A-8270 Semience	7 77.3 313 4 US-09-583-110-4236 Sequence	7 77.3 315 4 US-09-107-433-3706 Sequence	7 77.3 316 4 US-09-134-000C-4732 Sequence	7 77.3 334 4 US-09-710-279-10 Sequence	7 77.3 339 3 US-09-134-001C-3913 Sequence	7 77.3 341 3 US-09-134-001C-3568 Seguence	7 77.3 344 4 US-09-270-767-44219 Sequence	7 77.3 352 4 US-09-270-767-40279 Sequence 7 77.3 352 4 US-09-270-767-55495 Sequence	7 77.3 356 4 US-09-328-352-7671 Sequence	7 77.3 360 4 US-09-489-039A-13055 Sequence	//.3 360 4 05-09-581-110-1285 Sequence 77.3 361 4 US-09-107-433-3390 Sequence 77.3 361 4 US-09-107-433-3390 Sequence

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| Sequence 24, Application US/09911781
| Sequence 24, Application US/09911781
| Sequence 24, Application US/09911781
| Patent No. 6673613
| APPLICANT: Craft, David L.
| APPLICANT: Wilson, C. Ron
| APPLICANT: Eitich, Dudley
| APPLICANT: Eitich, Dudley
| APPLICANT: Eitich, Dudley
| TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
| FILE REFERENCE: U0012 OS/0AAP (1010-49)
| CURRENT APPLICATION NUMBER: US/09/911,781
| CURRENT APPLICATION NUMBER: 2001-07-24
| NUMBER OF SEQ ID NOS: 34
| SOO ID NO 24
| LENGTH: 267
| TYPE: PRT
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US-10-400-902-24

Sequence 24, Application US/10400902

Sequence 24, Application US/10400902

Patent No. 6790640

GENERAL INFORMATION:
APPLICANT: Carft, David L.
APPLICANT: Exich, Dudley
APPLICANT: Exich, Dudley
TITLE OF INVENTION: USE OF CYPEZAZA PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
TITLE OF INVENTION: USE OF CYPEZAZA PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT APPLICATION NUMBER: US/10/400,902

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: US/09/911,781

PRIOR FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 24
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APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHRONE P450 MONOXYGENASE AND NADPH CYTOCHRONE P450

TITLE OF INVENTION: CYTOCHRONE GENES AND PROTEINS RELATED TO THE OMEGA

TITLE OF INVENTION: HYDROXYLASC COMPLEX OF CANDIDA TROPICALIS AND METHODS

TITLE OF INVENTION: RELATING THERETO

FILE REFERENCE: 1010-16.seq

CURRENT APPLICATION NUMBER: US/09/302,620B

CURRENT PILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 109

SQOTWARE: Patentin Ver. 2.1

SEQ ID NO 106

LENGTH: 267

TYPE: PRT
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0; Mismatches 3; Indels
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US-09-302-620B-106
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US-09-911-781-24
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Sequence 119, App
Sequence 7553, Ap
Sequence 21641, A
Sequence 21, Appli
Sequence 21567, A
Sequence 24, Appli
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Sequence 27, Appli
Sequence 5971, Appli
Patent No. 5177197
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US-07-646-537B-2
US-09-538-022-932
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US-09-302-620B-106
Sequence 106, Application US/09302620B
Patent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Eritch, David L.
APPLICANT: Eritch, Dudley
APPLICANT: Behoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Cornett, Cathy A.
APPLICANT: Loper, John C.
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39 VTTTAEF 45
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                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                    1 VXXXAEF 7
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                                                                                                 ; SEQ ID NO:4:
; LENGTH: 268
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                                                                                                                                 5204252-4
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                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                TITLE OF INTERNATION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/386,837
FILING DATE: 27-JUL-1989
PRIOR APPLICATION NUMBER: 308
APPLICATION NUMBER: 308
FILING DATE: 08-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatent No. 5204252

APPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
FICATAGGIO, STEPHEN

TILLE OF INVENTION: CANDIDA TROFICALIS TRANSFORMATION SYSTEM
NUMBER OF SEQUENCES: 9
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Patent No. 5204252

PAPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA

PICATAGGIO, STEPHEN

TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

PILING DATE: 27-JUL-1989

PRIOR APPLICATION NUMBER: 308 481

FILING DATE: 08-FEB-1989
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                                                                                  Length 267;
                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                  ;Patent No. 5204252
; APPLICANT: CREGG, JAMES M.;GLEESON, MARTIN A.;HAAS, LISA
;PICATAGGIO, STEPHEN
                                                                                  Score 19; DB 4; I
Pred. No. 4.7e+02;
                                                                                                                 0; Mismatches
                                                                                86.4%;
57.1%;
             ; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-400-902-24
                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                  39 VITTAEF 45
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                                                                                                                                                 1 VXXXAEF 7
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LENGTH: 267
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5204252-2
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL GATY BRECON et. al
TITLE OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
FILLS OF INVENTION:
CURRENT APPLICATION NUMBER:
GENERAL FILLING DATE:
FILLS OF INVENTION:
FILLS OF INFORMATION:
FILLS OF INFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Rold, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
FILE REFERENCE: 11000.104101
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
: LENGTH: 179
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57.1%; Pred. No. 7.4e+02;
tive 0; Mismatches 3; Indels
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                                                              Length 89;
                                                              Score 18; DB 4; 1
Pred. No. 2.8e+02;
0; Mismatches 3,
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-634-238-296
; Sequence 296, Application US/09634238
Patent No. 6544772
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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, ORGANISM: Klebsiella pneumoniae
,US-09-489-039A-12873
                                                              Query Match 81.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                     82 VSNTAEF 88
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US-09-489-039A-12873
US-09-949-016-9298
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** APPLICATE VENTER, J. Craig et al.

** TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

** TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

** TILE DE INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

** CURRENT APPLICATION NUMBER: US/09/949,016

** CURRENT FILING DATE: 2000-04-14

** PRIOR PLILING DATE: 2000-10-20

** PRIOR PLILING DATE: 2000-10-03

** PRIOR PLILING DATE: 2000-09-08

** NUMBER OF SEQ ID NOS: 207012

** SOFTMARE: FastSEQ for Windows Version 4.0

** SEQ ID NO 9298

** LENGTH: 89
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                                                                                                                         , LOCATION: (55); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-288-143-158
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER FILE REFERENCE: 1703-021.US1
CURRENT APPLICATION NUMBER: US/09/410,132
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: 60/102,572
EARLIER FILING DATE: 1999-07-28
MUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN DATE: 1999-07-28
SOFTWARE: PATENTIN DATE: 1999-07-28
INDER OF SEQ ID NOS: 12
SEQ ID NO 4
IENGTH: 69
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Pred. No. 2.2e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                              Query Match 81.8%; Score 18; DB 4; Length 56; Best Local Similarity 57.1%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/09410132; Patent No. 6509458; GENERAL INFORMATION:
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Best Local Similarity 42.9
Matches 3; Conservative
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ORGANISM: Homo sapiens
                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VAARAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                  1 VXXXAEF 7
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ORGANISM: Human
                                                              FEATURE:
NAME/KEY: SITE
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US-09-949-016-9298
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US-09-410-132-4
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; Sequence 16774, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                          ; ORGANISM: Myxococcus xanthus
US-09-902-540-14188
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Petent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SPRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: JUN, Christopher

APPLICANT: HULTGREN, Scott J.

APPLICANT: HULTGREN, Scott J.

APPLICANT: HULTGREN, Scott J.

APPLICANT: HULTGREN, Christine A.

APPLICANT: EVANS, Amy K.

TITLE OF INVENTION: DECO PERIPLASMIC PROTEASE, A NEW ANTI-INFECTIVE TARGET

TITLE OF INVENTION: AND AN IN VITRO ASSAY FOR DEGP PROTEASE FUNCTION

FILE REFERENCE: 016921-149

CURRENT APPLICATION NUMBER: US/09/605,858

CURRENT FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PATENTIN VET. 2.0
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
                                                                                                                                ; Sequence 34, Application US/09605858 ; Patent No. 6306619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.8
Best Local Similarity 57.1
Matches 4; Conservative
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186 VVSTAEF 192
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ORGANISM: SpneumhtrA
US-09-605-858-34
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US-09-902-540-14188
                                                                                      RESULT 13
US-09-605-858-34
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LENGTH: 236
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Sequence 5099, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Parento or Diagnostics and Therapeutics
TITLE OF INVENTION: Parento or Diagnostics and Therapeutics
CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/081,533

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCOMPATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16774
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APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849)B

FULE REFERENCE: 38-10 (15849)B

CURRENT PELLING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR PILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 14188

LENGTH: 260
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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APPLICANT: POSTSYL, R. Allyn
APPLICANT: POSTSYL, R. Allyn
APPLICANT: Chisen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
FILE REFERENCE: ELITRA, 008A
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 346
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18326
LENGTH: 360
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Pred. No. 1.3e+03;
1; Mismatches 3;
                   PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 262
LENGTH: 338
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                                                                                                                                                                                                                                                                                                  ; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 346, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
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US-09-711-164-346
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Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                                                                                                                                                                                                         TYPE: PRT
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CURRENT APPLICANT: ON WUMBER: US/09/602,777A
CURRENT APPLICANT: DATE: 1999-0-6-2 APPLICANT: DATE: 1999-0-6-2 APPLICANT: DATE: 1999-0-7-0 APPLICANT: DATE: DAT
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                         Score 18; DB 4; Length 335;
Pred. No. 1.2e+03;
0; Mismatches 3; Indels
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                                                   TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-583-110-5099
                                                                                                                                                               81.8%;
57.1%;
                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                            224 VMSAAEF 230
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US-09-602-777A-262
SEQ ID NO 5099
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211 ISTTAEF 217

Wed Jun 15 09:21:18 2005

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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANTON: NUCLEIC Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: PARTHOO-07A
CURRENT APPLICANTON NUMBER: US 09/107,433
PRIOR APPLICANTON NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICANTON NUMBER: US 60/081,553
PRIOR APPLICANTON UNMBER: US 60/051,553
NUMBER OF SEQ ID NOS: 5322
LENGTH: 397
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US-09-107-433-4600
Sequence 4600, Application US/09107433
Sequence 4600, Application US/09107433
Patent No. 6800744
Setuence 4600, Application US/09107433
Sequence 4600, Application US/09107433
Sequence 4600, Application US/09107433
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.5e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                     Sequence 4402, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                          Sequence 15437, Application US/09902540
; Sequence 15437, Application US/09902540
; Patent No. 683347
; GENREAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Misgand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION: NUMBER: US/09/902,540
; CURRENT PLING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15437
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Sequence 2, Application US/09410132

Sequence 2, Application US/09410132

GENERAL INFORMATION:

APPLICANT: Haber, Baniel E.

APPLICANT: Mitchell, Stephen C.

TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 1703-001. US1

CURRENT APPLICATION NUMBER: US/09/410,132

CURRENT APPLICATION NUMBER: 60/102,572

SARLIER FILING DATE: 1999-09-30

SARLIER FILING DATE: 1999-09-30

SARLIER FILING DATE: 1999-09-30

SARLIER FILING DATE: 1999-07-28

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO. 2

LENGTH: 387

TYPE: PRT.
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81.8%; Score 18; DB 4; Length 387;
Best Local Similarity 42.9%; Pred. No. 1.40+03;
Matches 3; Conservative 1; Mismatches 3; Indels
                                                                       Score 18; DB 4; Length 360;
Pred. No. 1.3e+03;
                                                                                                                        3; Indels
                                                                                                                     0; Mismatches
                                                                     Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Myxococcus xanthus
, ORGANISM: Candida albicans
US-09-248-796A-18326
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Best Local Similarity 57.1
These 4: Conservative
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                                                                                                                                                                                                                    112 VITSAEF 118
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                                                                                                                                                                      1 VXXXAEF 7
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US-09-410-132-2
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FOR DIAGNOS

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Sequence 4, Application US/08973275B
; Sequence 4, Application US/08973275B
; Patent No. 5958706
; GENERAL INFORMATION:
    APPLICANT: MAMINA, Shinji
; APPLICANT: NAMINA, Shinji
; APPLICANT: NAMINA, Shinji
; TITLE OF INVENTION: PINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS
; TITLE OF INVENTION: PIEREPO, PROCESS FOR PRODUCING THE SAME, AND USE
; TITLE OF INVENTION: PIEREPO
; TITLE OF INVENTION: THEREPO
; TITLE OF INVENTION: THEREPO
; TITLE OF INVENTION: THEREPO
; TITLE OF INVENTION: UNBER: US/08/973,275B
; CURRENT TAPLICATION NUMBER: US/09/973,275B
; CURRENT FILING DATE: 1997-03-27
; EARLIER FILING DATE: 1997-03-27
; EARLIER FILING DATE: 1996-03-28
; EARLIER FILING DATE: 1996-03-28
; EARLIER FILING DATE: 1996-03-28
; EARLIER FILING DATE: 1996-05-16
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                                                                                                                                                                                                                                                                                                                                                                   Length 434;
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57.1%; Pred. No. 1.6e+03;
tive 0; Mismatches 3; Indels
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; Patent No. 6033878
; GENERAL INFORMATION:
APPLICANT: Tadashi MATSUNAGA
; TITLE OF INVENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: TRANSMEM
LOCATION: (7)..(380)
OTHER INFORWATION: Membrane bound region of mag A protein.
                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 2; Length 434 Pred. No. 1.6e+03; O; Mismatches 3; Indels
                       18-SEP-1995
                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,600I
FILING DATE: 18.5EP-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: UP 6-248700
FILING DATE: 16.5EP-1994
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       TOPE: anino acide TOPE: anino acide TOPE: anino acide OLECTE
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-529-600D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 VATLAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VATLAEF 63
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US-09-122-632-2
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ALD AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ALD AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SRIOR FILING DATE: 1999-01-29
SRO ID NO 10042
LENGTH: 403
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                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 4; Length 400; 57.1%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08529600D
Patent No. 5861285
GENERAL INFORMATION:
APPLICANT: Tadashi MATSUNAGA
TITLE OF INVENTION: PROTBIN-BOUND MAGNETIC PARTICLES AND
TITLE OF INVENTION: PROCESS OF PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...400
SEQUENCE DESCRIPTION: SEQ ID NO: 4600:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          LENGTH: 400 amino acids TYPE: amino acid
INFORMATION FOR SEQ ID NO: 4600:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                       SEQUENCE CHARACTERISTICS
                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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Matches 4; Conserv
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US-09-489-039A-10042
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US-08-529-600D-2
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Sequence 158, Application US/09684855
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US-09-684-855-158
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US-09-488-265B-23
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57.1%; Pred. No. 1.6e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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; Patent No. 6599735
; GENERAL INFORMATION:
APPLICANTON:
TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; TILE REFERENCE: C38435/11692
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 135
   PROCESS OF PRODUCING THE SAME
TITLE OF INVENTION: PROCESS OF PRODUCING THE S. NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/529,600
FILING DATE: 18-SEP-1995
APPLICATION NUMBER: JP 6-248700
FILING DATE: 16-SEP-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 annino acida
TYPE: amino acid
TYPE: amino acid
                                                                                                       COUNTRY: U.S.A.

ZIF: 20005-1918

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,632
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Best Local Similarity 57.1°
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-122-632-2
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CRGANISM: T. lanuginosa
US-09-684-855-135
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RESULT 30 US-09-684-855-158

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RESULT 32
US-09-328-352-7566
US-09-328-352-7566

Sequence 7566, Application US/09328352
Patent No. 656258
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 443
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Pred. No. 1.6e+03;
0; Mismatches 3; Indels
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Parent No. 6599735
GENERAL INFORMATION:
APPLICANT F. Hoffmann-La Roche AG
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/684.855
CURRENT APPLICATION NUMBER: 2000-10-06
PRIOR APPLICATION NUMBER: EP 90121663.9
PRIOR APPLICATION NUMBER: EP 99120289.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09488265B
Fatent No. 6720174
GENERAL INPORMATION:
APPLICANT: Lehmann, Martin
APPLICANT: Sonen
CURRENT APPLICATION NUMBER: US/09/488,265B
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 440
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.11
Local 4; Conservative
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TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESSE:
CITY: New York
STREET: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COUNTRY: U.S.A.
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: NEW COMPUTER: Diskette
COMPUTER: NEW COMPUTER: DISKETTE
COMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 3; L
Pred. No. 1.8e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Phytase Variants
TITLE OF INVENTION: Phytase Variants
FILE REPERENCE: $618.500.02
FURENT PELING 5618.500.03
CURRENT PELING DATE: 1999-03-22
RIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 0176
PRIOR APPLICATION NUMBER: PA 1999 0176
PRIOR APPLICATION NUMBER: PA 1999 0176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1998-01-37
PRIOR FILING DATE: 1998-06-25
NUMBER: 60/080,129
PRIOR FILING DATE: 1998-06-25
NUMBER: OF SEQ. 115-22
NUMBER: PAPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1998-06-25
NUMBER: OF SEQ. 115-22
NUMBER: PAPLICATION NUMBER: 60/090,675
NUMBER: PAPLICATION NUMBER: 60/090,675
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FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09273871A Patent No. 6514495 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REPERENCE/DOCKET NUMBER: 4758
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0238
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 VIASAEF 167
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SEQ ID NO 14
LENGTH: 475
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                                                                                                                                                  Gaps
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                                                                                Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BERKA, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 58661180 No. 5866118t of No. 5866118t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides Having Phytase Activity
                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New YORK
COMPUTRY: U.S.A.
ZIP: 10174-6401
COMPUTRER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DEMOCRACIA
COMPUTER: DEMOCRACIA
COPERATING SYSTEM: DOS
SOFTWARE: FASTESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 4758.200-US
REGISTRATION NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212 867 0123
TELEFRAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                         81.8%; Score 18; DB 4; I
57.1%; Pred. No. 1.6e+03;
iive 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 2; 1
57.1%; Pred. No. 1.8e+03;
tive 0; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09163642
Patent No. 6221644
SERENTAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides F.
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-819-825-2; Sequence 2, Application US/08819825; Patent No. 5866118; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                         Ouery Match
Best Local Similarity 57.1.
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein; FRAGMENT TYPE: internal US-08-819-825-2
                                                                                                                                                                                                                                                                            351 VAGTAÈF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 VIASAEF 167
                                                                                                                                                                                                             1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VXXXAEF 7
          US-09-328-352-7566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-163-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Gaps

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APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, RONALD F
APPLICANT: RUBGER, DAVID C
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: TUBERABANBATH, THANGAVEL
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OF MATTER
TITLE OF INVENTION: OF MATTER
                                                                                                                                                               Length 507;
                                                                                                                                                          Score 18; DB 4; Length 507
Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
ADDRESSEE: INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLUSSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/029,335
FILING DATE: 04-WAR-1993
PRIOR APPLICATION NUMBER: US 07/971,091
FILING DATE: 03-NOV-1992
PRIOR APPLICATION NUMBER: US 07/946,235
FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: US 07/938,336
FILING DATE: 08-MG-1992
PRIOR APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-UL-1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND RESISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRP-081CP
                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-459-346-19; Sequence 19, Application US/08459346; Patent No. 5834179; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CINFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 amino acids
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                 1 VXXXAEF 7
; SEQ ID NO 11504
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11504
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Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 08/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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                                                                                                      Query Match 81.8%; Score 18; DB 4; Length 475; Best Local Similarity 57.1%; Pred. No. 1.8e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.8%; Score 18; DB 4; Length 475; Best Local Similarity 57.1%; Pred. No. 1.8e+03; Matches 4; Conservative 0; Mismatches 3; Indela
                                                                                                                                                                                                                                                                                                                                          US-10-083-452-14

Sequence 14, Application US/10083452

Patent No. 668938

GENERAL INFORMATION:
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618-500-US

CURRENT FILING DATE: 2002-02-26

PRIOR PELLOATION NUMBER: US/10/083,452

CURRENT FILING DATE: 1999-03-22

PRIOR FILING DATE: 1998-03-23

PRIOR FILING DATE: 1998-03-23

PRIOR FILING DATE: 1998-06-19

PRIOR FILING DATE: 1998-00-10-22

PRIOR APPLICATION NUMBER: PA 1998 00106

PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: PA 1999 00091

PRIOR FILING DATE: 1998-01-22

PRIOR FILING DATE: 1998-01-22

PRIOR PRILING DATE: 1998-01-22

PRIOR FILING DATE: 1998-01-22

PRIOR FILING DATE: 1998-01-22

PRIOR FILING DATE: 1998-01-32

PRIOR FILING DATE: 1998-01-32

PRIOR PRILING DATE: 1998-06-25

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 14

SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosa
US-09-273-871A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Thermomyces lanuginosa
                                                                                                                                                                                                                                                              161 VIASAEF 167
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APPLICANT: Israel, David
Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
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                                          APPLICANT: JONES, WILLIAM K
APPLICANT: JONES, RONALD F
APPLICANT: TUCKER, RONALD F
APPLICANT: OFFERNANN, HERMANN
APPLICANT: OFFERNANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: NUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: OF MATTER
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 3; Length 513;
Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MCDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,419
FILING DATE: 08-UUL-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/459,346
FILING DATE: O2-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOWAS C.
REGISTRATION NUMBER: 36,989
REFERENCY/DOCKET NUMBER: CRP-081DVCN
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
TENTIH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMP6 (HUMAN)"
PUBLICATION INFORMATION:
AUTHORS: CELESTE,
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, Testa, Hurwitz
ADDRESSEE: Thibeault, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08469411
Patent No. 6190880
GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
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DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                     USA
      Patent No. 6071708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-889-419-19
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-469-411-8
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Sequence 8. Application US/07989847
Patent No. 5866364
GENERAL INFORMATION:
APPLICANT: Israel, David
APPLICANT: Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                      Length 513;
                                              /note= "PRE-PRO-BMP6 (HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
                                                                                                                                                                                                                                    Score 18; DB 2; ]
Pred. No. 1.9e+03;
0; Mismatches 3
NAME/KEY: Protein
LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMP
PUBLICATION INFORMATION:
AUTHORS: CELESTE,
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: KADINGS, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEPAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 19, Application US/08889419
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Best Local Similarity 57.1
Ellines 4; Conservative
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-07-989-847-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 436
                                                                                                                                           ; PAGES: 9843-9847
; DATE: 1991
US-08-459-346-19
                                                                                                                                                                                                                                                                                                                                                                  250 VVTAAEF 256
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US-08-889-419-19
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US-07-989-847-8
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LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMP
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                       FILING DATE: 08/029,335
PRIOR APPLICATION NUMBER: US 08/029,335
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,091
FILING DATE: 03-MOV-1992
PRIOR APPLICATION NUMBER: US 07/946,235
FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: US 07/938,336
FILING DATE: 08-AUG-1992
PRIOR APPLICATION NUMBER: US 07/938,336
FILING DATE: 31-JUL-1992
ATTORNEY AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REPRENCE/DOCKET NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REPRENCE/DOCKET NUMBER: 27,820
   APPLICATION NUMBER: US/08/040,510
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MOLECULE TYPE: protein
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DATE: 1991
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Matches
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APPLICANT: TUCKER, RONALD F
APPLICANT: TUCKER, RONALD F
APPLICANT: TUCKER, DAYLD C
APPLICANT: TUCKER, DAYLD C
APPLICANT: OFFENAN, HERNANN
APPLICANT: OFFENAN, ENGIN
APPLICANT: OFFENAN, ENGIN
APPLICANT: OFFENAN, ENGIN
APPLICANT: OF INVENTION: OF MATTER
TITLE OF INVENTION: OF MATTER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
ADDRESSEE: 1NC.
STRRET: 35 SOUTH STREET
CITY: HOPKINTON
                                                      ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.8%; Score 18; DB 3; Length 513; Best Local Similarity 57.1%; Pred. No. 1.9e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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ZIP: 01748
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-402-542-19; Sequence 19, Application US/08402542; Patent No. 6395883; GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 VVTAÄEF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VXXXAEF 7
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Sequence 8, Application US/09780601A; Sequence 8, Application US/09780601A; Sequence 8, Application US/09780601A; Sequence 8, Application US/09780601A; Patent No. 6593109; GENERAL INFORMATION:

APPLICANT: Israel, David APPLICANT: Wolfman, well M.

TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

STREET: ADDRESSE: Legal Affairs, Genetics Institute, Inc.

STREET: 87 Cambridge Park Drive COUNTY: Cambridge Park Drive COUNTY: Tape COUNTY: Tape COUNTY: Tape COUNTY: Tape COMPUTER READABLE FORM:

MEDIUM TYPE: Tape COMPUTER: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/780,601A; FILING DATE:
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                 81.8%; Score 18; DB 3; Length 513; 57.1%; Pred. No. 1.9e+03; ive 0; Mismatches 3; Indels
/notes "PRE-PRO-BMP6 (HUMAN)"
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PATEUR NO. 518 V.V.O.

PAPPLICANT: WOZNEY, JOHN M.; WANG, ELIZABETH A.; ROSEN, VICKI A.; CELESTE, ANTHONY J.

TILLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS NUMBER OF SEQUENCES. 16

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/490,033

FILING DATE: O7-MAR-1990

PRIOR APPLICATION NUMBER: 370,544

FILING DATE: O7-MAR-1989

APPLICATION NUMBER: 370,559

FILING DATE: 23-JUN-1989

APPLICATION NUMBER: 179,100

FILING DATE: 08-APR-1988

APPLICATION NUMBER: 179,100

FILING DATE: 08-APR-1988

APPLICATION NUMBER: 179,101

FILING DATE: O8-APR-1988

APPLICATION NUMBER: 179,197
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Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                       COMPOUTE TATACABLE FORM:

COMPOUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATM:
APPLICATION NUMBER: PCT/US93/07189
FILING DATE: 19930729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..513 /note= "PRE-PRO-BMP!
OTHER INFORMATION:
PUBLICATION:
AUTHORS: CELESTE,
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT:
NAME: KELLEY, ROBIN D.
REGIESTATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-1
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE GIARACTERISTICS:
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APPLICATION NUMBER: 28,285
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
STREET: 35 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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DATE: 1991
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                                                                                                                                 USA
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                                                                                                                                      COUNTRY:
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOD.307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 513;
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Pred. No. 1.9e+03;
0; Mismatches 3;
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             PULDADILLATION
PULDADILLATION
PURD APPLICATION DATA:
APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
ATTORNEY AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B-CON
TELECOMMUNICATION INFORMATION:
TELEFRHOME: 617-489-8622
TELEFRHOME: 617-876-5851
INFORMATION FOR SEQ ID NO: 8: SEQUENCE GHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
TYPE: amino acids
TYPE: ACCOUNT ACCOUN
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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US-09-949-016-6118
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PCT-US93-07189-19
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LENGTH: 513
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CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 VITAÄEF 309
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: C1001307
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;Patent No. 5187076
; APPLICANT: WOZNEY, JOHN M.;WANG, ELIZABETH A.;ROSEN,VICKI A.;
;CELESTE, ANTHONY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELESTE, ANTHONY J.

TITLE ANTHONY J.

NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/490,033
FILING DATE: 07-MAR-1990
APPLICATION NUMBER: 347,559
FILING DATE: 28-MAR-1989
APPLICATION NUMBER: 329,610
FILING DATE: 28-MAR-1989
APPLICATION NUMBER: 329,610
FILING DATE: 08-MAR-1989
APPLICATION NUMBER: 179,100
FILING DATE: 08-MAR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 08-ARR-1988
APPLICATION NUMBER: 13,346
FILING DATE: 26-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 10-DEC-1986
                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 6; Length 513; 57.1%; Pred. No. 1.9e+03; ive 0; Mismatches 3; Indels
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FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
APPLICATION NUMBER: 943,322
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 880,776
FILING DATE: 01-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-JUL-1986
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Best Local Similarity 57.1-
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Best Local Similarity 57.1
Matches 4; Conservative
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US-09-949-016-10103
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                                                                                                                                                                                                                                   LENGTH: 513
                                                                                                                                                                                                        SEQ ID NO:6:
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Sequence 12, Application US/09828302

Patent No. 6818805

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: CHITANI, MANABU

TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

TITLE OF INVENTION UNMBER: 60/196,001

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 12

LENGTH 532
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Sequence 11259, Application US/09949016

Sequence 11259, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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Pred. No. 2e+03;
0; Mismatches 3; Indels
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CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10103
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Batent No. 6335182

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
APPLICATION:
FILE REPERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347

CURRENT PILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 660
                                                                                                                                                                                                                                                                                                            105-09-268-347-46
| Sequence 46, Application US/09268347
| Sequence 46, Application US/09268347
| Patent No. 6335182
| GENERAL INFORMATION:
| APPLICANT: LOOSMORE, Sheena M. |
| TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS FILE REPREBRUE: 1038-860
| CURRENT APPLICATION UNBER: 1999-03-16
| NUMBER OF SEQ ID NOS: 54
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 46
| LENGTH: 659
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                                                                                                                Score 18; DB 4; Length 637;
Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 3; Length 659; Pred. No. 2.5e+03; 0; Mismatches 3; Indels
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US-002-252-991A-31488
'Sequence 31489, Application US/09252991A
'Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Haemophilus influenzae US-09-268-347-46
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                         TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                           213 VALSAEF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 VASNAEF 579
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                                                                               US-09-543-681A-5869
    SEQ ID NO 5869
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                         LENGTH: 637
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Patent No. 6605709
GENERAL INFORMATION:
ADELICANT: GARY BESTON
TITLE OF INVENTION: UDIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF PAPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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APPLICANT: Wen, Taui-Juna
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl Coa Levels in Plants
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                                                                                                                                                                                                     DB 4; Length 563;
                                                                                                                                                                                                   81.8%; Score 18; DB 4; Length 563
57.1%; Pred. No. 2.1e+03;
tive 0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11259
LENGTH: 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 201573
CURRENT APPLICATION NUMBER: US/09/344,882
CURRENT PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/090,717
PRIOR FILING DATE: 1998-06-26
SEQ ID NOS: 38
SOFTWARE: PATENTIN VEY: 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09344882; Patent No. 6764851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nikolau, Basil J
Wurtele, Eve S
Oliver, David J
Behal, Robert
Schnable, Patrick S
Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Arabidopsis Thaliana
                                                                                                                                                                                 Ouery Match
Best Local Similarity 57.1.
4; Conservative
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Matches 4; Conservative
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                                                                                                                                         ORGANISM: Human
US-09-949-016-11259
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US-09-543-681A-5869
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US-09-344-882-18
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LENGTH: 607
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 12, Application US/08772270A

Patent No. 6019984

GENERAL INFORMATION:
APPLICANT: MacInnes, Janet
APPLICANT: Ricciatii, Paul
APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                          US-09-083-587-2
; Sequence 2, Application US/09083587
; Sequence 2, Application US/09083587
; Patent No. 6492188
; GENERAL INFORMATION:
; APPLICANT: Schmandt, et al.
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 18; DB 4; Length 672; 57.1%; Pred. No. 2.6e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6340
TELEFAX: (312) 474-6340
TELEFAX: (312) 474-6348
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
DESCRIPTION: /desc = "hPAL peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Bereskin & Parr
40 King Street West
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Matches 4; Conservative
471 VRTSAEF 477
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CLASSIFICATION:
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US-08-772-270A-12
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               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION OF 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 18; DB 4; Length 669; illarity 57.1%; Pred. No. 2.6e+03; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 18; DB 3; Length 672; 57.1%; Pred. No. 2.6e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COLOUGH, DOBVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
DESCRIPTION: /desc = "hPAL peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 672 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.13
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 VYAAAEF 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-363-708-2
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Gaps

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Redmond, Mark J.
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US-09-248-796A-16379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-295
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 VSSDAEF 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VXXXAEF 7
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                          94025
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                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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US-09-569-037-8
US-09-569-037-8
i Sequence B, Application US/09569037
i Patent No. 6753151
i GENERAL INFORMATION:
i APPLICANT: Jackson, Stephen P
i APPLICANT: Gell, David A
i TITLE OF INVENITON: thereof
i TILL REPERBLUCE: 620-100
i CURRENT APPLICATION NUMBER: US/09/569,037
i CURRENT FILING DATE: 2000-05-11
i PRIOR FILING DATE: 2000-03-31
i PRIOR FILING DATE: 1999-04-01
i NUMBER OF SEQ ID NOS: 18
i SOUTWARE: PatentIn Ver. 2.1
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                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/772,270A

FILING DATE: December 23, 1996

CLASSIFICATION: 424

ATTONREY/AGENT INPORMATION:

NAME: Gravelle, Micheline

REGISTRATION NUMBER: 40,261

REGISTRATION NUMBER: 6580-81

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION OF SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 amino acids

TTOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/07603133B ; Patent No. 5298244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-569-037-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.17
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 4; Conservative
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 VLSAAEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718 VANAAEF 724
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US-07-603-133B-12
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Sequence 16379, Application US/09248796A

Factor 1904-1807, Application US/09248796A

Factor No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PEDLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409

REOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16379

LENGTH: 1010
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APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 1; Length 775; Pred. No. 3e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODING, RODERTE 13,208
REGISCHATION NUMBER: 33,208
REGISCHATION NUMBER: 9313-0004.00
TELECHMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 4;
Pred. No. 4e+03;
                                                                                                                                                                     ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                              COMPUTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN FRE-BOS #1.0, Version #1.30B
SOFTWARE: PARENTING POSTEM: 10.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
MAME: PARKET, David
REGISTRATION NUMBER: UMIC:002
FELECOMMUNICATION INFORMATION:
TELEPRONCE (512) 320-720
TELEFRANC: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
'LONGTH: 1252 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08316650; Patent No. 5942496; GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Rosesler, Blake J.
APPLICANT: Goldstein, Steven A.
TITLE OF INVENTION: Washan
TITLE OF INVENTION: FOR STIMULATING BONE CELLS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941 VYSSAEF 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                  CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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  Gaps
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                                                                                                                                                                                                                                                                                            APPLICANT:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING BONE
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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Patent No. 5763416
GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Goldstein, Steven A.
TITLE OF INVENTION: And Tissues
TITLE OF INVENTION: And Tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:

STATE:

COUNTRY:

COUNTRY:

CONDUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER:

MEDIUM TYPE:

COMPUTER:

MEDIUM TYPE:

CONDUTER:

SOFTWARE:

SOFTWARE:

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

APPLICATION:

PRIOR APPLICATION:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

MAME:

PRESTATION NUMBER:

TELENAMINICATION INFORMATION:

MAME:

PRESTATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELEFAX:

T
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 18; 57.1%; Pred. No. 5
                                                                                                                                                                                         RESULT 62
PCT-0895-02251-3
PSequence 3, Application PC/TUS9502251
GENERAL INFORMATION:
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                           621 VITEAEF 627
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                                                    1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
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US-08-199-780-3
Matches
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                       Score 18; DB 3; Length 1253;
Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLUM TYRE: FLODPY GISK

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/592,685

FILING DATE: 12-Jun-2000

CLASSIFCATION: cUnknown>
PRIOR APPLICATION NUMBER: US/08/479,722B

APPLICATION NUMBER: US/08/479,722B

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US PCT/US95/02251

FILING DATE: 21-FBB-1995

APPLICATION NUMBER: US 08/316,650

FILING DATE: 30-SEP-1994

APPLICATION NUMBER: US 08/199,780

FILING DATE: 18-FBB-1994

ATTORNEY/AGENT INFORMATION:

NAMMS: FUSSEY Shelley P.M.

REGISTRATION NUMBER: 39,458

REGISTRATION NUMBER: 39,458

REGISTRATION NUMBER: 39,458
                                                                                                                                                                                                                                                                  Sequence 4, Application US/09592685

Patent No. 6774105

GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Wuchan
TITLE OF INVENTION: LATENT TGF ( BINDING PROTEIN (LTBP)
GENES, COMPOSITIONS AND METHODS
                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Williams, Morgan & Amerson STREET: 7676 Hillmont, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: Linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-592-685-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 67
US-09-077-098A-7
; Sequence 7, Application US/09077098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 77040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (713) 934-7011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                           Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1-
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 VYSSAEF 947
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                                                                                                              1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; Length 1252;
Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08479722B
Patent No. 6074840
GENERAL INFORMATION
APPLICANT: Vin, Wushan
TITLE OF INVENTION: LATENT TOF( BINDING PROTEIN (LTBP)
TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: 1628

ZIP: 77040

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,722B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
FILING DATE: 30-FEB-1994
FILING DATE: 30-FEP-1994
FILING DATE: 30-FEP-1994
FILING DATE: 18-FEB-1994
ATORNEY AGENT INFORMATION
NAME: REGISTRATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
ATORNEY AGENT INFORMATION:
NAME: FURSEY, Shelley P. M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
TELEPHONE: (713) 934-7001
TELEPHONE: (713) 934-7011
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Williams, Morgan & Amerson 7676 Hillmont, Suite 250
                    REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC:008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELER: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1252 amino acids
TYPE: amino acid
Parker, David L.
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear; MOLECULE TYPE: protein US-08-479-7228-4
                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-316-650-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         941 VYSSAEF 947
                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF 7
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STREET: 7676 H.
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                TOPOLOGY:
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US-08-479-722B-4
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US-09-34-016-6978

Sequence 6978, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINDOWS Version 4.0

SEQ ID NO 6978

LENTH: 4377
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APPLICANT: Tang, Jordan J.N.
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Koelsch, Gatald
TITLE OF INVENTION: Gatalytically Active Recombinant Memapsin and Methods
TITLE OF INVENTION: Gatald
TITLE OF INVENTION: Gatald
TITLE OF INVENTION: Go Use Thereof
TITLE OF INVENTION: Of Use Thereof
TITLE OF INVENTION: Of Use Thereof
TITLE OF INVENTION: Of Use Thereof
TITLE OF INVENTION NUMBER: Go/141,363
PRIOR APPLICATION NUMBER: Go/141,363
PRIOR APPLICATION NUMBER: Go/141,363
PRIOR APPLICATION NUMBER: Go/177,836
PRIOR APPLICATION NUMBER: Go/177,836
PRIOR APPLICATION NUMBER: Go/177,836
PRIOR PAPLICATION NUMBER: Go/177,836
PRIOR PAPLICATION NUMBER: Go/177,836
PRIOR PAPLICATION NUMBER: Go/177,836
PRIOR PAPLICATION NUMBER: Go/118,368
PRIOR APPLICATION NUMBER: Go/210,292
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Pred. No. 1.9e+04;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                    Length 3913;
                                                                                                                                                                                                                                                                                                    Score 18; DB 4; Length 391
Pred. No. 1.7e+04;
1; Mismatches 3; Indels
                                  NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10933

LENGTH: 3913

TYPE: PRT

ORGANISM: Human
US-09-949-016-10933
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                                                                                                                                                                                                                                                                                                       81.8%;
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2933 IATTAEF 2939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3397 IATTAÈF 3403
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APPLICANT: Tang, J
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-6978
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Sequence 10933, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

FITLE OF INVENTION:

TITLE OF IN
Patent No. 6544519

GENERAL INFORMATION:
GENERAL TOKUNAGA, Eiji
SARAGUCHI, Maeashi
MATSUO, Kalaburo
HAMADA, Fukusaburo
TOKLYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURROITER KEALMALE CANNINGER
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
CORRENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098A
FILING DATE: 19-May-1998
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAME: KORNBAU, Anne
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2039;
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                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 4; I
Pred. No. 8.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2039 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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US-09-949-016-10933
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Gaps

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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 57.1
Matches 4; Conservative
                      atsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-724-566A-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; TITLE OF INVENTION: of Use Thereof
; TITLE OF INVENTION: of Use Thereof
; TITLE OF INVENTION: of Use 179
; CURRENT FILING DATE: 2000-06-27
; PRIOR FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-11-30
; PRIOR PILING DATE: 1999-11-30
; PRIOR PILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
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                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-604-608-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors US-09-604-608-28
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                                                                                                                                                                                                                                                                                 3; Indels
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                                                                                                                                                                                                                                    Score 17; DB 4; Length 7; Pred. No. 4.1e+05; 0; Mismatches 3; Indels
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Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: AAGERSON, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Power, Michael
                                                                                                                                                                                                                                    77.3%;
57.1%;
PRIOR FILING DATE: 2000-06-08
                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                                      PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 8
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Best Local Similarity 57.1°
                                                                                                                                                                                                                                 Query Match 77.3
Best Local Similarity 57.1
Matches 4; Conservative
                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 27
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US-09-724-566A-87
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US-09-604-608-28
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APPLICANT: Tatesuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwa
APPLICANT: Wang, Shuwa
ITILE OF INVENTION: Meta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT FILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-02-10
PRIOR PILING DATE: 1999-06-10
PRIOR PILING DATE: 1999-06-15
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 220-15-NBWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
FRIOR APPLICATION NUMBER: 60/139,172
FRIOR PILING DATE: 1999-06-15
NUMBER: OF SEQ ID NOS: 104
SEQ ID NO 87
LENGTH: 9
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APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Sinha, Sukanto
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FEATURE:
OTHER INFORMATION: APP fragment
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Gaps
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## APPLICANT: Tung, Jay
## APPLICANT: Tung, Jay
## APPLICANT: Tung, Jay
## APPLICANT: McConlogue, Lisa
## TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
## TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
## TITLE OF INVENTION: Methods
## FILE REFERENCE: 228-US-NEWC2
CURRENT FAPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
## PRIOR APPLICATION NUMBER: US 09/501,708
## PRIOR PILING DATE: 1999-02-10
## PRIOR FILING DATE: 1999-02-10
## PRIOR FILING DATE: 1999-06-15
## NUMBER OF SEQ ID NOS: 104
## SOFTWARE: FastSEQ for Windows Version 4.0
## LENGTH: 9
## CONTRACT: DOTALLED
## CONTRACT: DOTALED
## CONTRACT: DOTALLED
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77.3%; Score 17; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels
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                    CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1990-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1990-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 9
   CURRENT APPLICATION NUMBER: US/09/724,566A
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APPLICANT: Anderson, John P.
APPLICANT: Baas, Guriqbal
APPLICANT: Boas, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Fower, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Gwen
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US-09-724-566A-94
'Sequence 94, Application US/09724566A
'Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: APP fragment
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APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Beta-Secretase
TITLE OF INVENTION: WHERE: US/09/724,566A
CURRENT APPLICATION NUMBER: US/09/501,708
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
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APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
      Pred. No. 4.1e+05;
0; Mismatches 3; Indels
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SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 9
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US-09-724-566A-89
; Sequence 89, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
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PATENT No. 6627739
APPLICANT: Anderson, John P. APPLICANT: Dane, Minh Tam APPLICANT: Done, Minh Tam APPLICANT: Prigon, No. 6627739mand
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
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ORGANISM: Artificial Sequence
57.1%;
   Best Local Similarity 57.1 Matches 4; Conservative
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Matches 4; Conservative
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Sinha, Sukanto
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US-09-724-566A-93
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APPLICANT:
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PRIOR PAPLICATION NUMBER: US 60/114,408
PRIOR FILING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 89
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Doane, Minh Tam
Frigon, No. 6830918mand
John, Varghese
Power, Michael
Sinha, Sukanto
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Sequence 93, Application US/09471669A
Patent No. 6830918
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 89, Application US/09471669A Patent No. 6830918 GENERAL INFORMATION:
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Tung, Jay
Wang, Shuwen
McConlogue, Lisa
Elan Pharmaceuticals, .
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Similarity 57.1%;
4; Conservative C
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 9
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Wang, Shuwen
APPLICANT: Blan Pharmaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270-006430US
CURRENT APPLICATION NUMBER: US 60/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-31
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR PRILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARRE: PATENTIN VET: 2.1
LENACTH: 0
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US-09-471-669A-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Ban Pharmaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REPREBUCE: 015270-006430US
CURRENT APPLICATION NUMBER: US,09/471,669A
PRIOR APPLICATION NUMBER: US,60/114,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-12-31
APPLICATION NUMBER: US 60/119,571
FILING DATE: 1999-02-10
APPLICATION NUMBER: US 60/139,172
FILING DATE: 1999-06-15
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APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
APPLICANT: John, Varghese
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                  APPLICANT: Anderson, John P.
APPLICANT: Basi, Guridbal
APPLICANT: Doane, Minh Tam
APPLICANT: Prigon, No. 6830918mand
APPLICANT: John, Varghese
APPLICANT: Sower, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                Sequence 87, Application US/09471669A; Patent No. 6830918; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 88, Application US/09471669A
; Patent No. 6830918
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Best Local Similarity
Matches 4; Conserv
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Gaps
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-88
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// OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-89
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CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION TOWNER: US/09/471,669A
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                                                                                                                            Length 9;
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Pred. No. 4.1e+05;
0; Mismatches 3; Indels
                                                                                                                        Score 17; DB 4; I
Pred. No. 4.1e+05;
0; Mismatches 3;
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MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage COMPUTER: PC OPERATING SYSTEM: DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
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Sequence 12.751.12
Sequence 10. 564372
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
TITLE OF INVENTION: POLYPEPFIDES BI
TITLE OF INVENTION: CRYPTOSPORIDIUM
TITLE OF INVENTION: APPLICAN TITLE OF INVENTION: NETHODS FOR INM
TITLE OF INVENTION: METHODS FOR INM
TITLE OF INVENTION: METHODS FOR INM
TITLE OF INVENTION: DIAGNOSIS AND K
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
STREET: 385 Sherman Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
: United States of America
                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09634955B Patent No. 6511834
GENERAL INFORMATION:
                                             77.3%;
57.1%;
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Best Local Similarity 57.1-
---- 4; Conservative
                                                                                         4; Conservative
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                                           Query Match
Best Local Similarity
Matches 4; Conserv
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STATE: Californ
                                                                                                                                  1 VXXXAEP 7
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  US-09-471-669A-94
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US-08-415-751-12
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OTHER INFORMATION: Description of Artificial Sequence: APP fragment
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US-09-471-669A-93
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PELICANT: Tatsunc,
PELICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
APPLICANT: McConlogue, Lisa
APPLICANT: Elan Pharmaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270-006430US
FILE REFERENCE: 015270-006430US
FILE REFERENCE: 015270-006430US
FILE REFERENCE: 015270-006430US
FILE REFERENCE: 01999-12-24
                                                                                                             APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
APPLICANT: Elan Pharmaceuticals, Inc.
APPLICANT: Elan Pharmaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270-006430US
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 9
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CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
SOFTWARE: PATENTIN VOR: 2.1
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APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
APPLICANT: John, Varghese
Frigon, No. 6830918mand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Sinha, Sukanto
Tatsuno, Gwen
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Best Local Similarity 57.1
Matches 4; Conservative
                                           Power, Michael
Sinha, Sukanto
                      John, Varghese
                                                                                       Tatsuno, Gwen
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APPLICANT:
APPLICANT:
  APPLICANT:
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APPLICANT: Meyers, Rachel
APPLICANT: COOK, William James
TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-134
CURRENT APPLICATION NUMBER: US/09/634,955B
CURRENT FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.
LENGTH: 23
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Score 17; DB 4; Length 9; Pred. No. 4.1e+05; 0; Mismatches 3; Indels
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APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERBYCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR RILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NO 7973
LENGTH: 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH;
; LENA, HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH PACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENA; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLECTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
HUMBER OF SEQUENCES: 27-1000 DATA:
FILING DATE: 27-1000 DATE:
FILING DATE: 27-1000 DATE:
                                                                                                                                                                                                                                                                                                                                                          Length 68;
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Pred. No. 4.3e+02;
0; Mismatches 3;
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Pred. No. 4.3e+02;
0; Mismatches 3
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57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-543-681A-7973
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
4; Conserve
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;Patent No. 5177197
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5177197-52
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US-09-248-796A-24127, Application US/09248796A

Sequence 24127, Application US/09248796A

Sequence 24127, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: WCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANT: TITLE OF INVENTION: WOLEST AND THERAPEUTICS

TITLE OF INVENTION: WOLEST ACID AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION WHERE: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR PELING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 24127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.3%; Score 17; DB 1; Length 47; 57.1%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Positions coded by nonsense codons are NAME/KEY: identified as Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.3%; Score 17; DB 4; 1
57.1%; Pred. No. 4.1e+02;
tive 0; Mismatches 3,
           FILING DATE: 03.4PR-1995
CLASSIFICATION: 435
PRIOR DATE: 05.4PR-1995
FILING DATE: 06.071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07.891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
REGISTRATION NUMBER: 30.518
REGISTRATION NUMBER: 480.19-2 (HHD)
TELECOMMUNICATION INFORMATION:
TELEPPAN: (415) 324-1677
TELEPPAN: (415) 47-1677
TELENTH: 47 amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-543-681A-7973
; Sequence 7973, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VELAÄEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 VKIAAEF 60
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Best Local Similarity
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Matches 4; Conserv
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Sequence 27, Application US/08479078

Sequence 27, Application US/08479078

Patent No. 5814466

GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: Method for Assaying for a Substance that
TITLE OF INVENTION: Method for Assaying for a Substance that
TITLE OF INVENTION: Method for Assaying for a Substance that
TITLE OF INVENTION: Affects an SH2-Phosphorylated Ligand Regulatory System
NUMBER OF SEQUENCES: 27
CORRESPONDER EADBESS: AREA OF STATE: Ontario
COUNTRY: Canada
ZIP: M5H 372
COUNTRY: Canada
ZIP: M5H 372
COMPUTER READBESE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-311-731A-185

Sequence 185, Application US/08311731A

Patent No. 658326A

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: SMITH, DOUGLAS

TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                Length 95;
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                                                                                                                                                                      3; Indels
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Pred. No. 6.2e+02;
0; Mismatches 3;
                                                                                                           Score 17; DB 4; I
Pred. No. 6.1e+02;
0; Mismatches 3;
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                   Query Match
Best Local Similarity 57.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                    36 VRDAAEF 42
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                                                  US-08-311-731A-79
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                                                     Sequence 16536, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

FILE REFERENCE: 107196.132

PRIOR RPELICATION NUMBER: US 60/074,725

PRIOR PELICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79, Application US/08311731A

Patent No. 658326

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: SMITH, DOUGLAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS: 411

CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

STREET: ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
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LENGTH: 95 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.3
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 VMKAAEF 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-311-731A-79
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OP SEQUENCES: 87
CORRESPONDENCE SLED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98104-702
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.3%; Score 17; DB 4; I 42.9%; Pred. No. 8.1e+02; tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5330:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc_feature
) LOCATION: (B) LÖCATION 1...122
) SEQUENCE DESCRIPTION: SEQ ID NO: 5330:
US-09-107-532A-5330
                                                                                         GTC-012
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Application US/09183861
Patent No. 6365165
                       ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILLEFAX: (206) 682-6031
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 ITDTÄËF 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-183-861-49
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                        COUNTRY: USAN

ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
RECESTRATION NUMBER: 31,616
REFERENCE/DOCKET: 31,616
REFERENCE/DOCKET: 31,616
REFERENCE/DOCKET: 11720-2441
TELEPHONE: 617/720-2441
STELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
TENDYTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Masaachusetts
COUNTRY: USA
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/085,598
APPLICATION NUMBER: 60/051571
                     NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                         CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-09-107-532A-5330
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                                                                                                                                                     COUNTRY:
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1 VXXXAEF 7
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Patent No. 6375955
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reados-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skalky, Yasir A.W.
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES:
ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                77.3%; Score 17; DB 3; Length 136; 57.1%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEADLING NOWENDS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILLING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Washington
COUNTRY: USA
ZIP. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAWNE: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPANE: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                         ; ORGANISM: Leishmania chagasi
US-09-183-861-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Leishmania chagasi
US-09-022-765-49
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
           STRANDEDNESS: single
TOPOLOGY: linear
                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
amino acid
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RESULT 95

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JOSEPH SECONDARY APPLICATION US/09551974A

SEQUENCE 49, APPLICATION US/09551974A

PATENT NO. 6500437

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dillon, Davin R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-565-501A-49

i Sequence 49, Application US/09565501A

j Sequence 40. 660731

j GENERAL INFORMATION:
   APPLICANT: Campos-Neto, Antonio
   APPLICANT: Campos-Neto, Antonio
   APPLICANT: Billion Davin C.
   APPLICANT: Billion Davin C.
   APPLICANT: Bhatia, Ajay
   APPLICANT: Beter Probst
   TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
   TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
   FILE REFERENCE: 210121.420C6
   CURRENT APPLICATION NUMBER: US/09/565,501A
   WIMMED OR SECOTT NAME: 22000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 136;
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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; LENGTH: 136
; TYPE: PRT
; ORGANISM: Leishmania chagasi
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 49
LENGTH: 136
TYPE: PROGRANISM: Leishmania chagasi
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Patent No. 6517156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
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           APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Coler, Ralea
APPLICANT: Probst, Peter
ITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.4207
CURRENT FAPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 136
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APPLICANT: Brobst, Peter

APPLICANT: Brobst, Peter

APPLICANT: Brannon, Mark

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

TITLE REFERENCE: 210121-420C8

CURRENT APPLICATION NUMBER: US/09/874,923

CURRENT APPLICATION NUMBER: 2001-06-04

NUMBER OF SEQ ID NOS: 122

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 49

LENGTH: 136

TYPE: PRT

CORGANISM: Leishmania chagasi
US-09-874-923-49
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
                                                                                                                                                                                                                                                                                                                                                                                                                            77.38;
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ORGANISM: Leishmania chagasi
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Best Local Similarity 57.3
Matches 4; Conservative
Webb, John R.
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US-09-874-923-49
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Sequence 14343, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG

TITLE OF INVENTION: NUMBER: US/09/248,796A

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13

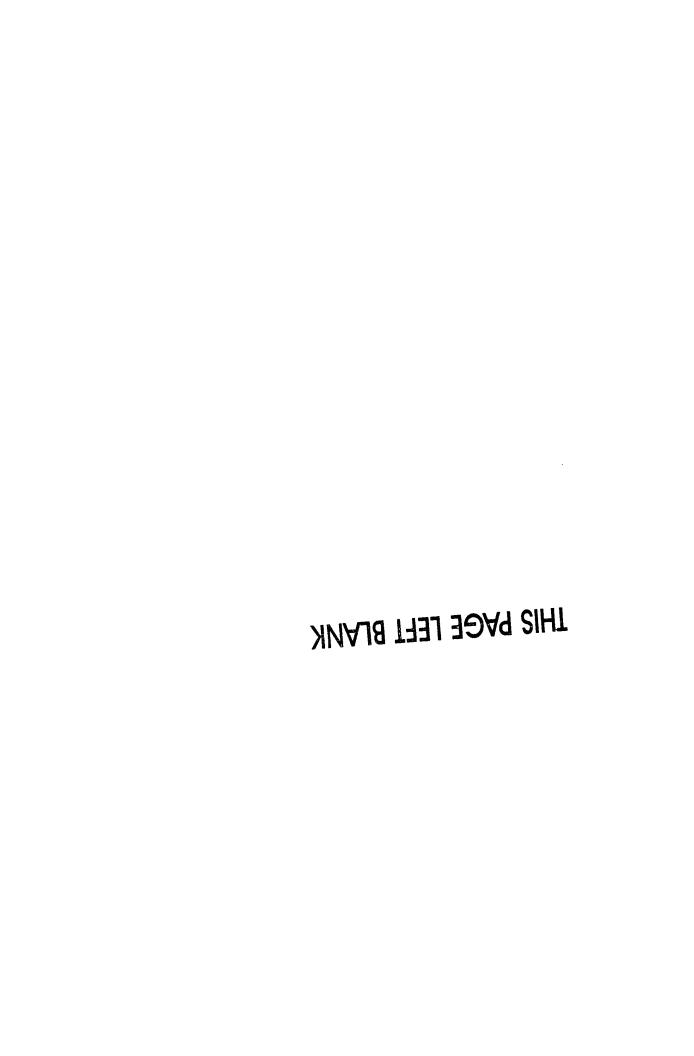
PRIOR PELING DATE: 1998-02-13

PRIOR PELING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14343

LENGTH: 143
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 13, 2005, 14:00:46 Job time : 34 secs
                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Enterococcus faecalis US-09-134-000C-4544
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Sequence 106, App Sequence 106, App Sequence 10732, A Sequence 302302, Sequence 72638, A Sequence 2, App 1 Sequence 57008, A Sequence 57008, A Sequence 51691, A Sequence 51691, A Sequence 7569, A Sequence 6737, App Sequence 6737, App

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1 US-10-139-218-106
1 US-10-400-902-24
1 US-10-400-902-24
1 US-10-418-898-106
1 US-10-138-898-106
1 US-10-282-121-10242
1 US-10-282-121-2-3-56631
1 US-10-282-122A-72638
1 US-10-282-122A-72638
2 US-10-282-122A-72638
2 US-10-282-122A-72638
2 US-10-282-122A-72638
2 US-10-282-122A-72639
2 US-10-282-122A-72649
3 US-10-425-115-23739
3 US-10-425-115-273915
3 US-10-425-11
      App
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Sequence 161742,
Sequence 361705,
Sequence 24, Appl
Sequence 106, App
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                                                                                                  June 13, 2005, 14:00:08; Search time 109 Seconds (without alignments) 24.618 Million cell updates/sec
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Published Advisor Bright Published Advisor Breining A
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                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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6 US-10-437-963-161742

6 US-10-437-963-126883

6 US-10-425-115-361705

US-09-911-781-24

US-09-916-800-106

4 US-10-138-838-106

4 US-10-138-905-106

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4 US-10-139-296-106
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Maximum Match 100%
Listing first 300 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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267
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Post-processing:

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Perfect score:

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Sequence:

Scoring table:

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Searched:

Sequence 228254, Sequence 49255, A Sequence 10066, A Sequence 255955, Sequence 190652, Sequence 14633, Sequence 144633, Sequence 271612, Sequence 271612, Sequence 271612, Sequence 271601, Sequence 33400, A Sequence 33400, A

4, Appli 228254,

237245, 243983, 275053,

Sequence Sequence Sequence Sequence

Sequence 390, App Sequence 61704, A Sequence 274236, Sequence 16985, Sequence 16932, A Sequence 24773, Sequence 24533, Sequence 64341, A Sequence 64341, A Sequence 6199, App Sequence 199, App Sequence 199, App

228146, 274885,

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241928, 241928, 271613, 1165533, 121186,

Sequence Sequence Sequence

Sequence Sequence 247828, 98, Appl 262409,

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Query Match

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52 16 US- 55 17 US- 56 15 US- 58 9 US- 59 16 US- 68 15 US- 68 15 US- 68 15 US- 71 15 US-	88 15 US- 93 16 US- 101 15 US- 112 15 US- 115 15 US- 116 15 US- 116 15 US- 116 US- 117 US- 118 US- 118 US- 119	33 15 US-10-282-122A-62445 33 15 US-10-282-122A-63915 33 15 US-10-282-122A-64921 34 14 US-10-481-265-73 34 15 US-10-481-265-73 34 15 US-10-425-114-44807 35 9 US-09-815-242-13346 35 15 US-10-425-114-44807 35 15 US-10-425-114-44807 35 15 US-10-425-1138 35 17 US-10-472-928-1738 36 US-09-738-626-6959 43 15 US-10-369-493-11820 44 US-10-287-243-41820	15 US-10-389-566-2148 17 US-10-72-923-10163 15 US-10-72-923-110163 17 US-10-369-493-17473 17 US-10-424-599-28498 16 US-10-424-599-28498 16 US-10-424-599-28498 15 US-10-434-56114 15 US-10-334-5614-2 16 US-10-345-5614-2 17 US-10-282-1224-74248 18 US-10-282-1224-74248 19 US-10-282-1224-74248 11 US-10-282-1224-7209	05 17 US-10-732-923-1030 18 15 US-10-352-923-1030 18 15 US-10-369-493-12707 25 16 US-10-369-493-12707 40 15 US-10-442-538-158 47 15 US-10-442-538-158 47 15 US-10-369-493-4845 57 14 US-10-369-493-23726 67 17 US-10-325-939-2 67 17 US-10-325-939-2 67 17 US-10-732-923-23726 67 17 US-10-734-510-4 68 19 US-09-738-626-6986 89 19 US-09-738-626-6986 81 US-10-369-493-5201 85 15 US-10-369-493-5201 85 15 US-10-369-493-5201 85 17 US-10-369-493-5201 85 17 US-10-369-493-5201 86 18 US-10-282-122A-53682 80 115 US-10-282-122A-53682 80 116 US-10-437-963-150846
1.8 252 16 US- 1.8 253 17 US- 1.8 256 15 US- 1.8 258 16 US- 1.8 258 16 US- 1.8 258 15 US- 1.8 268 15 US-	1.8 288 15 US- 1.8 293 16 US- 1.8 301 15 US- 1.8 312 15 US- 1.8 315 15 US- 1.8 323 15 US- 1.8 324 17 US- 1.8 324 15 US- 1.8 323 15 US- 1.8 323 15 US- 1.8 323 15 US- 1.8 323 15 US- 1.8 324 15 US- 1.8 324 15 US- 1.8 324 15 US- 1.8 324 15 US- 1.8 325 15 US- 1.8 326 15 US- 1.8 327 US- 1.8 328 15 US- 1	1.8 333 15 US-10-882-122A-62445 1.8 333 15 US-10-282-122A-63915 1.8 333 16 US-10-282-122A-64921 1.8 334 14 US-10-16-86-76-8848 1.8 334 15 US-10-481-265-73 1.8 335 15 US-10-425-114-44807 1.8 335 15 US-10-425-114-44807 1.8 335 15 US-10-425-11346 1.8 335 17 US-10-472-926-1738 1.8 335 17 US-10-472-926-18912 1.8 347 14 US-10-287-2746-346	1.8 349 15 US-10-389-566-2148 3.6 15 US-10-732-923-10163 1.8 368 17 US-10-7282-1224-55895 1.8 368 17 US-10-282-124-599-2849 1.8 369 15 US-10-424-599-284982 1.8 371 9 US-09-78-62-6691 1.8 378 16 US-10-424-599-284982 1.8 379 15 US-10-34-564-174114 1.8 397 15 US-10-34-564-8 1.8 397 15 US-10-282-1224-74248 1.8 397 17 US-09-769-744-152 1.8 397 17 US-10-282-1224-74248 1.8 397 17 US-10-282-1224-7428 1.8 402 15 US-10-282-1224-72509 1.8 402 15 US-10-282-1224-72509	05 17 US-10-732-923-1030 18 15 US-10-352-923-1030 18 15 US-10-369-493-12707 25 16 US-10-369-493-12707 40 15 US-10-442-538-158 47 15 US-10-442-538-158 47 15 US-10-369-493-4845 57 14 US-10-369-493-23726 67 17 US-10-325-939-2 67 17 US-10-325-939-2 67 17 US-10-732-923-23726 67 17 US-10-734-510-4 68 19 US-09-738-626-6986 89 19 US-09-738-626-6986 81 US-10-369-493-5201 85 15 US-10-369-493-5201 85 15 US-10-369-493-5201 85 17 US-10-369-493-5201 85 17 US-10-369-493-5201 86 18 US-10-282-122A-53682 80 115 US-10-282-122A-53682 80 116 US-10-437-963-150846

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NESULT 1
US-10-437-963-200225
US-10-437-963-200225
Sequence 200225, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Branzuk, Brad
APPLICANT: Branzuk, Brad
APPLICANT: Branzuk, Brad
APPLICANT: Li Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Rice Nucleic Acid Molecules
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 200225
LENGTH: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ed Rosa, Thomas J.
APPLICANT: Ed Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 161742
LENGTH: 130
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Pred. No. 1e+03;
0; Mismatches 3; Indels
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US-10-437-963-161742
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LOCATION: (1)..(130)
PERTINER INFORMATION: unsure at all Xaa locations
PEATURE:
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Sequence 161742, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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Sequence 199286,
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Sequence 199386,
Sequence 308930,
Sequence 308930,
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Sequence 46, Appl
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Sequence 51, Appl
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Sequence 53, Appl
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Sequence 63, Appl
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Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
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Sequence 28, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 57, Appl
Sequence 58, Appl
Sequence 24, Appl
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US-10-474-599-199286
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APPLICANT: Trang, Maria
APPLICANT: Trang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Geneson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUC
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CFI
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REPERENCE: 1010-12
CURRENT APPLICATION NUMBER: US/09/976,800
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
                                           Sequence 24, Application US/09911781
Patent No. US20020034788A1
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Birich, Dudley
APPLICANT: Application USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REPERENCE: U0012 OS/0AAP (1010-49)
CURRENT APPLICATION NUMBER: US/09/911,781
CURRENT PILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
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SEQ ID NO 24
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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US-09-976-800-106
S Gequence 106, Application US/09976800
Publication No. US20030077795A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Eirich, Budley
APPLICANT: Eshoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Benner, Alfred A.
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US-10-138-838-106
S. Sequence 106, Application US/10138838
Publication No. US20030049821A1
GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Candida tropicalis
US-09-911-781-24
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; ORGANISM: CANDIDATROPICALIS
US-09-976-800-106
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                                                                                                                                          Sequence 126883, Application US/10437963
; Bublication No. US20040123343A1
; Bublication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Acvalic, David K.
; APPLICANT: Acvalic, David K.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENITON: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENITON: 18-21 (53221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: La Rosa Thereof for Plant Improvement
; FLLE REFERENCE: 38-21 (53221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: La Rosa Thereof for Plant Improvement
; ELE REFERENCE: 38-21 (53221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
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86.4%; Score 19; DB 16; Length 241;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 19; DB 16; Length 146; 57.1%; Pred. No. 1.1e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_29387C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_93051C.1.pep
US-10-425-115-361705
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 241
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Matches 4; Conservative
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ORGANISM: Oryza sativa
                                                36 VSASAEF 42
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ORGANISM: Zea mays
1 VXXXAEF
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                                                                                                                               RESULT 3
US-10-437-963-126883
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GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C^I TROPICALIS AND METHODS RELATING THERETO
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APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUI
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C.
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,916
DURRENT APPLICATION DATE: 2002-05-03
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CURRENT APPLICATION NUMBER: US/10/138, 905
CURRENT FILING DATE: 2002-05-03
PRIOR PAPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SSOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: 09/976, 800
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/302,602
PRIOR FILING DATE: 1999-04-30
                                                                                                                                S-10-138-905-106
Sequence 106, Application US/10138905
Publication No. US20030068800A1
GENERAL INFORMATION:
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Publication No. US20030073220A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Erich, Dudley
APPLICANT: Bshoo, Mark
APPLICANT: Maddari, Krishna M.
APPLICANT: Corrett, Cathy A.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                           APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.4%;
Best Local Similarity 57.1%;
Matches 4; Conservative 0
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Loper, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                 Tang, Maria
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39 VTTTAEF 45
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                                                                                          APPLICANT: Madduri, Krishna M.
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Gleeson, Martin
TILE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GRESS AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
TITLE OF INVENTION: GRESS AND METHODS RELATING THERETO
TITLE OF INVENTION: GRESS AND METHODS RELATING THERETO
TITLE OF INVENTION: UNMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOUTHWARE OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Maria
TITLE OF INVENTION: CYTOCHROME F450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTAGE
TITLE OF INVENTION: TROPICALIS AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF (FILE REPERENCE: 1010-16
CURRENT PRILICATION NUMBER: US/10/139,031
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR PILING DATE: 2000-10-10-1
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eritch, Dudley.
APPLICANT: Bshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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57.1%;
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NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
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57.1%;
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ORGANISM: CANDIDATROPICALIS
Wilson, Ron C.
Craft, David L.
Eirich, Dudley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: CANDIDATROPICALIS
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Best Local Similarity 57.13
Terhes 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                             Eshoo, Mark
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SEQ ID NO 106

1 VXXXAEF 7

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APPLICANT: LODGE, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CTYOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUC
TITLE OF INVENTION: GREES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wilson, C. Ron
APPLICANT: Birich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REPERENCE: U0012 OS/OAAP (1010-49)
CURRENT APPLICATION NUMBER: US/10/400, 902
CURRENT APPLICATION NUMBER: US/09/911, 781
PRIOR APPLICATION NUMBER: US/09/911, 781
PRIOR PLING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
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Pred. No. 2.1e+03;
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    TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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                 FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
FRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SENGTH: 267
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PUblication No. US20030186411A1
GENERAL INPORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Wilson, Ron C.
APPLICANT: Erich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Behoo, Mark
APPLICANT: Behoo, Mark
APPLICANT: Benoor, Cathy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 24, Application US/10400902
; Publication No. US20030175896A1
GENERAL INFORMATION:
; APPLICANT: Craft, David L.
                                                                                                                                                                                                                                                                                                                                       86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Candida tropicalis
US-10-400-902-24
                                                                                                                                                                                                                                                                  ; ORGANISM: CANDIDATROPICALIS
US-10-139-218-106
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Best Local Similarity 57.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 VTTTÄEF 45
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Graft, David L.
APPLICANT: Elich, Dudley
APPLICANT: Elicho, Mark
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Green, John C.
APPLICANT: Tang, Maria
APPLICANT: Gleen, Maria
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICANTON NUMBER: US/10/139, 296
CURRENT APPLICANTON NUMBER: US/10/139, 296
CURRENT APPLICANTON NUMBER: US/10/976, 800
PRIOR APPLICANTON NUMBER: US/09/976, 800
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APPLICANT: Madduri, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Glesson, Martin
TITLE OF INVENTION: CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF (
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                                                                                                                                                                     3; Indels
                                                                                                                      Score 19; DB 14;
Pred. No. 2.1e+03;
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Sequence 106, Application US/10139296 Publication No. US20030148486A1 GENERAL INFORMATION:
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                                                                                                                      86.4%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
; LENGTH: 267
; TYPE: PRT
; ORGANISM: CANDIDATROFICALIS
US-10-138-916-106
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                     4; Conservative
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Best Local Similarity
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Best Local Similarity
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US-10-139-296-106
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APPLICANT:
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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         APPLICANT: Carr, Grant U.

APPLICANT: Yanamoto, Robert T.

APPLICANT: Yanamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Probaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/206,848

PRIOR PLICATION NUMBER: 60/206,848

PRIOR PLICATION NUMBER: 60/206,848

PRIOR PLICATION NUMBER: 60/206,848

PRIOR PLICATION NUMBER: 60/207,777

PRIOR APPLICATION NUMBER: 60/207,779

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-12-22

PRIOR PLILNG DATE: 2000-12-22

PRIOR PLILNG DATE: 2000-12-16

PRIOR PLILNG DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 10242

LENGTH: 298
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Pred. No. 2.3e+03
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-815-242-10242
Carr, Grant J.
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Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 VSTTÁÈF 178
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APPLICANT:
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APPLICANT: Brenner, Alfred A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Toper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME F450 MONCOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDORENER RELATED TO THE OMEGA HYDROXYLASE COMPLEX
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: UNDOINGER: US/10/138, 898
CURRENT APPLICATION NUMBER: US/09/976, 800
PRIOR FILING DATE: 2001-10-12
CURRENT PAPLICATION NUMBER: US/09/976, 800
SPRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SSQ ID NO 106
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                CURRENT APPLICATION NUMBER: US/10/405,660
CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
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Patent No. US20020061569A1;
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert;
APPLICANT: Ohlsen, Kari L.;
APPLICANT: Zyskind, Judith W.;
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 106, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1
Matches 4; Conservative
FILE REFERENCE: 1010-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VTTTAEF 45
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US-09-815-242-10242
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US-10-138-898-106
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PELING DATE: 2003-02-20
FRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,335
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2001-02-16
PRIOR DATE: 2
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Publication No. US20050106588A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: B5688;
CURRENT APPLICATION NUMBER: US/10/888,656
CURRENT APPLICATION NUMBER: 2004-07-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 355
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Pred. No. 2.8e+03;
0; Mismatches 3;
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US-10-425-114-57008
; Sequence 57008, Application US/10425114
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORGANISM: Papaver somniferum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 VATAÁÉF 232
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US-10-888-656-2
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; Sequence 302302, Application US/10425115
; Publication No. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Solution NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 302302
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
LENGTH: 298
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US-10-425-115-302302
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Tyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Tawick, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Escherichia coli
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Best Local Similarity 57.1°
...nes 4; Conservative
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Matches 4; Conservative
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US-10-425-115-302302
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Gaps

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Page 9

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: NuCleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: 105/10/425,115
CURRENT PILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 336689
LENGTH: 747
TYPE: ...
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NOS: 73128
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Pred. No. 5.8e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_70192C.1.pep
US-10-425-115-336689
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Best Local Similarity 57.1%;
Matches 4; Conservative
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APPLICANT: Zhou, Yihua
APPLICANT: Scoren, Steven K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
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ORGANISM: Zea mays
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Baukharov, Andrey A.

APPLICANT: Baukharov, Andrey A.

APPLICANT: Baubazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILS REFERENCE: 38-21(53221)

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 128132

LENGTH: 586
                                                                                                                                                                                               APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Correct Steven E
APPLICANT: A Sociated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57008
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US-10-425-114-57008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 128132, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
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                                                                                                                                                         Publication No. US20040034888A1
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Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-128132
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APPLICANT: Syskind, Judith
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanoro, Robert
APPLICANT: Yamanoro, Y
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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US-10-425-114-62401
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Pred. No. 5.9e+03;
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FILE REFERENCE: 30-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62401
LENGTH: 751
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57.1%;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local Similarity 57.1
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Best Local Similarity
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 1266
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Sequence 6737, Application US/10369493
; Bedication No. US2003023367541
; BedneRL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Gaiter, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; FILE REFERENCE: 38-10(52052)8
; CURRENT APPLICATION NUMBER: US 40/360,039
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.4%; Score 19; DB 17; Length 1584; Best Local Similarity 57.1%; Pred. No. 1.2e+04; Matches 4; Conservative 0; Mismatches 3; Indels
  Indels
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  Mismatches
                                                                                                                                                                               US-10-489-740-173

Sequence 173, Application US/10489740

PUblication No. US20050112574A1

GENERAL INFORMATION:

APPLICANT: Bionomics Limited

TITLE OF INVENTION: P9

FILE REFERENCE: Anglogenesis PCT

CURRENT APPLICATION NUMBER: US/10/489,740

CURRENT FILING DATE: 2004-03-15

NUMBER OF SEQ ID NOS: 216

SOFTHARE: PatentIn version 3.1

SEQ ID NO 173

LENGTH: 1584
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; Sequence 48, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Caenorhabditis elegans US-10-369-493-6737
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1549 VSAAAĖF 1555
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                                             1 VXXXAEF 7
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 212707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_340C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158, Application US/09984429
Publication No. US20040010132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,591
FRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 14;
Pred. No. 1.8e+02;
0; Mismatches 3;
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Pred. No. 7.3e+02;
0; Mismatches 3
              CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
FRIOR APPLICATION NUMBER: US 60/275,756
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 212707, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic peptide US-10-032-818-54
                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
FILE REFERENCE: 2932.1006-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 VVSTAEF 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                    FEATURE:
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; Sequence 49, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 292-1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR PILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEC 1D NOS: 83
; SOFTWARE: FastSEQ for Windows Version 4.0
                APPLICANT: Ghosh, Arun K.

7 ITILE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 293-1006-007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT APPLICATION NUMBER: US/10/032,818
FRIOR PRIOR PILING DATE: 2001-12-28
FRIOR PRIOR PELING DATE: 2001-03-14
FRIOR PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 12
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APPLICANT: Koelsch, Gerald
APPLICANT: Ghosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.8%; Score 18; DB 14; Length 12; Best Local Similarity 57.1%; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 14; Length 12;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Synthetic peptide US-10-032-818-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic peptide US-10-032-818-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 54, Application US/10032818; Publication No. US20030092629A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
Koelsch, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1°
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US-10-032-818-49
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LENGTH: 12
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57.1%; Pred. No. 8.3e+02; ative 0; Mismatches 3;
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57.1%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
     Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                              36 VAARAEF 42
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                                                                                        1 VXXXAEF 7
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ORGANISM: Zea mays
FEATURE:
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ORGANISM: Zea mays
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US-10-425-115-237245
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US-10-425-115-243983
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-150-111-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . LOCATION: (55)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-984-429-158
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81.8%; Score 18; DB 11; Length 56;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
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Publication No. US20030078386A1

GENERAL INFORMATION:

APPLICANT: Rubin et al.

TITLE OF INVENTION: Secreted Protein HPEAD48

FILE REFERENCE: PZ048HD1

CURRENT APPLICATION NUMBER: US/10/150,111

CURRENT APPLICATION NUMBER: 05/288,143

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-10-09

PRIOR APPLICATION NUMBER: 60/061,463

PRIOR APPLICATION NUMBER: 60/061,529

PRIOR PILING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR PILING DATE: 1997-10-09
PRIOR PELING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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LENGTH: 56
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Sequence 243983, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: APPLICANT: Arou, Yihua
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 243983
LENGTH: 61
Sequence 237245, Application US/10425115
Sequence 237245, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With APPLICANT: Applicant: Plants
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 237245
LENGTH: 60
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Pred. No. 9e+02;
0; Mismatches 3; Indels
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US-10-425-115-237245
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US-10-425-115-243983
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Pred. No. 9.1e+02;
0; Mismatches 3
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RESULT 37

Score 18; DB 14; Length 56;

81.8%;

Query Match

09730329-59ed.rapb

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...cutCANT: Cao Yohua
TITLE OF INVENTION: Soy. Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy. Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION WOMBER: 105/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 228254
LENGTH: 86
TYPE. T
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US-10-369-493-10066

Sequence 10066, Application US/10369493

Fublication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Gladman, Barry S.

APPLICANT: Glandman, Barry S.

APPLICANT: Glater, Xianfeng

TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERIUS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES

TITLE OF UNDENTION: PLANTS WITH IMPROVED PROPERIES

CURRENT APPLICATION NUMBER: US/10/369,493
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: DAILS 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49255
LENGTH: 91
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                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_48141C.1.pep
US-10-44-599-228254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 15; L Pred. No. 1.3e+03; O; Mismatches 3;
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57.1%; Pred. No. 1.4e+03;
cive 0; Mismatches 3.
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US-10-425-114-49255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49255, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 VTSOAEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 VLSTAEF 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF
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                                                                                                                                               Sequence 27563, Application US/10425115
Fublication No. US20040214272A1
Fublication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwal K.
APPLICANT: Zhou, Xihua
APPLICANT: Cao, Yongwal K.
APPLICANT: APPLICANT Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 275653
LENGTH: 66
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER FILE REFERENCE: 511582003110
CURRENT APPLICATION NUMBER: US/10/334,561A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: 09/410,132
PRIOR APPLICATION NUMBER: 60/146,584
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 18; DB 16; Length 66; 57.1%; Pred. No. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE;
; OTHER INFORMATION: Clone ID: MRT4577_182439C.1.pep
US-10-425-115-275053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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GENERAL INFORMATION: APPLICANT: La Rosa Thomas J
RAPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/10334561A; Publication No. US20030211520A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VAAYAEF 65
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
US-10-424-599-228254
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US-10-334-561A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-334-561A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Sequence 326590, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REPRENCE: 38-21(5222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 326590

LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                    Sequence 190652, Application US/10425115
| Sequence 190652, Application US/10425115
| Publication No. US2004021427241
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Cao, Yonguei
| APPLICANT: Cao, Yonguei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants |
| TI
Score 18; DB 16; Length 100;
Pred. No. 1.5e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 81.8%; Score 18; DB 16; Length 102; Best Local Similarity 57.1%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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; OTHER INFORMATION: Clone ID: MRT4577_105452C.1.pep
US-10-425-115-190652
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US-10-425-115-326590
          81.8%;
57.1%;
      Query Match 81.8
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                       1 VXXXAEF 7
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                                                                                                                         41 VSVSAEF
                                                                                                                                                                                                                                                                                                           RESULT 44
US-10-425-115-190652
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US-10-767-701-53633
is Sequence 53633, Application US/10767701
is Publication No. US20040172684A1
is GENERAL INFORMATION:
is APPLICANT: Shou, Yihua
is APPLICANT: Cao, Yongwai
is TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
if TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
is FILE REFERENCE: 38-21 (53535) B
is CURRENT FILING DATE: 2004-01-29
is NUMBER OF SEQ ID NOS: 63128
is SEQ ID NO 53633
in IENGTH: 95
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: About Yihua
APPLICANT: APPLICANT: And Yihua
APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                      81.8%; Score 18; DB 15; Length 93; 57.1%; Pred. No. 1.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: MRT4577_165021C.1.pep
US-10-425-115-255955
                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: 13468723.pep
US-10-767-701-53633
   CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10066
LENGTH: 93
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Best Local Similarity 57.1°
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 VRTAÄEF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 VITSAEF 85
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 43
US-10-425-115-255955
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WS-10-424-599-156801

Sequence 156801, Application US/10424599

Sequence 156801, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 274994, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: 18-21222B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 274994
                                                             APPLICANT: In COMBANCE TO BOOK TO BE APPLICANT: A ROSA, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: APPLICANT: Cao, Yingwei TITLE OF INVENTION: Dlants TITLE OF INVENTION: Plants FILE OF INVENTION: Plants FILE OF INVENTION: Plants FILE OF INVENTION: DLATE: 18-21(53222)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 271612 LENGTH: 122
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US-10-425-115-274994
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57.1%; Pred. No. 1.8e+03;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: MRT4577_179303C.1.pep
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81.8%; Score 18; DB 16;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3;
Sequence 271612, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1-
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                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exposition of K
APPLICANT: Shou Yihua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 144633
LENGTH: 121
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
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US-10-424-599-144633
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US-10-437-963-184577
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(121)
OTHER INFORMATION: unsure at all Xaa locations
                     ; Sequence 144633, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 184577, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
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RESULT 48

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1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                US-10-425-115-297969
                                                                                                                                                                                                                                                                             RESULT 53
US-10-425-115-238741
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Sequence 297969, Application US/10425115

Sequence 297969, Application US/10425115

Sequence 297969, Application US/2040214272A1

Sequence 297969, Application NS/2040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 297969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Other Molecules Associated With
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US-10-767-701-33440

i Sequence 33440, Application US/10767701

i Publication No. US20040172684A1

i GENERAL INFORMATION:

i APPLICANT: Kovalic, David K.

i APPLICANT: Zhou, Yingwei

i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa

i TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

i FILE REFERENCE: 38-21(5335) B

i CURRENT APPLICATION NUMBER: US/10/767,701

i NUMBER OF SEQ ID NOS: 63128

i SEQ ID NO 33440

i LENGTH: 124
    Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 81.8%; Score 18; DB 16; Length 124; Similarity 57.1%; Pred. No. 1.9e+03; 4; Conservative 0; Mismatches 3; Indels
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US-10-767-701-33440
                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_112613C.1.pep
US-10-424-599-156801
TITLE OF INVENTION: Plants and Uses There FILE REPERENCE: 38-21(5/223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 124
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Best Local Similarity 57.1°
"-hea 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                    ORGANISM: Glycine max
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Best Local Similarity
Matches 4, Conserva
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ORGANISM: Zea mays
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Sequence 228146, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 39-21(5323)8
CURRENT PLILNG DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 222146
LENGTH: 129
                                                                                                                                                                                                                                                                                                            Sequence 218974.1. Application US/10425115

Sequence 21874.1. Application No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: La Rosa, Thomas J.
APPLICANT: Acoalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION:
PILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: 2003-04-28
CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

LENGTH: 125
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                                                                  Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 125;
                                                                                                                   3; Indels
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US-10-424-599-228146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_14931C.1.pep
US-10-425-115-238741
OTHER INFORMATION: Clone ID: MRT4577_34819C.1.pep
                                                               Query Match 81.8%; Score 18; DB 16;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 3;
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Best Local Similarity 57.1.
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                                                                                                                                                                                                              112 VTARAEF 118
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                               APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Goo, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53315) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61704
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: In CONTINUE AND AND APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: APPLICANT: APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE OF INVENTION: Plants FILE OF INVENTION: Plants INS/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 274236 LENGTH: 142
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Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
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US-10-425-114-61704
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US-10-425-115-274236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 16;
57.1%; Pred. No. 2.1e+03;
iive 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 274236, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1
Local 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 58
US-10-425-115-274236
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US-10-424-599-279916
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                                                                                 Sequence 274885.
Sequence 274885.
Sequence 274885. Application US/10424599
Sequence 274885. Application Wo. USCO040031072A1
Sequence 274885. Application No. USCO040031072A1
SEQUENCE 274885.
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APPLICANT: JACKMAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.1e+03;
0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 18; DB 15; Length 137; 57.1%; Pred. No. 2.1e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90241C.1.pep
US-10-424-599-274885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/370,715B CURRENT FILING DATE: 2003-02-21 NUMBER OF SEQ ID NOS: 742 SEQ ID NO 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 61704, Application US/10425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 390, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patin Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 VAAEAEF 109
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  33 VAVAAEF 39
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US-10-425-114-61704
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Sequence 16932, Application US/10369493
; Sequence 16932, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TILLE REPERENCE: 38-10 (52052)8
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16932
. LENGTH: 159
                                                                                    APPLICANT: Barbazuk, Brad Applicant: Brad Applicant: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBNCE: 38-21(53221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 198547 LENGTH: 155
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APPLICANT: LA ROVALIC David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_94196C.1.pep
US-10-437-963-198547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 16;
Pred. No. 2.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.8%; Score 18; DB 15; Best Local Similarity 57.1%; Pred. No. 2.4e+03; Matches 4; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 234753, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Caulobacter crescentus US-10-369-493-16932
                                                                          Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Oryza sativa
    Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 VAAEAEF 148
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                                                                             APPLICANT:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabauk, Brad
APPLICANT: Brabauk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 16968
LENGTH: 149
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 144
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42.9%; Pred. No. 2.2e+03;
tive 1; Mismatches 3; Indels
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US-10-437-963-169685
                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_94788C.1.pep
US-10-424-599-279916
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                  LOCATION: (1)..(144)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
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133 IATAAEF 139
                                                                                                                                                                                          ORGANISM: Glycine max
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NAME/KEY: ungure
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Pred. No. 2.6e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                            Indels
                                                                     OTHER INFORMATION: Clone ID: LIB3632-058-F7_FLI.pep
                                                                                                                                                              Score 18; DB 15; L
Pred. No. 2.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7611
LENGTH: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-156-761-7611
Sequence 7611, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces avermitilis US-10-156-761-7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-199
                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                         57 VTRAAEF 63
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      ORGANISM: Zea mays
                                                                                                      US-10-425-114-64341
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| Sequence 245373, Application US/10424599 |
| Sequence 245373, Application US/10424599 |
| Publication No. US20040031072A1 |
| GENERAL INFORMATION: |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: Zhou Yihua |
| APPLICANT: Cao Yongwei |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION NUMBER: US/10/424,599 |
| CURRENT APPLICATION NUMBER: US/10/424,599 |
| NUMBER OF SEQ ID NOS: 285684 |
| SEQ ID NO 245373 |
| LENGTH: 165
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Publication No. US2004003488A1

Publication No. US2004003488A1

GAPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Availc, David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabas
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Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_54009C.1.pep
US-10-424-599-234753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_63602C.1.pep
US-10-424-599-245373
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234753
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                    Query Match

81.8%;

Best Local Similarity 57.1%;

Matches 4; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 VAARAEF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 WASAEF 151
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Matches 4; Conserv
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LENGTH: 167
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                                                                                                                                                                                                                                                             FEATURE:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(53223)
ETILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162790
LENGTH: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2003-04-28
KUMBER OF SEQ ID NOS: 369326
SEQ ID NO 241928
LENGTH: 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_118017C.1.pep
US-10-424-599-162790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 15; Le
Pred. No. 2.8e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_152217C.1.pep
US-10-425-115-241928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 16;
Pred. No. 2.8e+03;
0; Mismatches 3;
                                                                                                                                     US-10-424-599-162790
; Sequence 162790, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 241928, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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US-10-156-761-9937
; Sequence 9937, Application US/10156761
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                          11 VSGAÄEF 17
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                  1 VXXXAEF 7
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FEATURE:
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                                                                                                                                                                                  Sequence 40084, Application US/10767701
Sequence 40084, Application US/10767701
Sequence 40084, Application US. US2040172684A1
GENERAL INFORMATION:
David K.
Septicant: Zhou, Yongwei
TITLE OF INVENTION: David K.
TITLE OF INVENTION: David Molecules and Other Molecules Associated With
TITLE OF INVENTION: David K.
TITLE OF INVENTION: David K.
TITLE OF SEQUID NOS: 63128
SEQUID NO 40084
LENGTH: 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.8%; Score 18; DB 16; Length 187; Best Local Similarity 57.1%; Pred. No. 2.8e+03; Matches 4; Conservative 0; Mismatches 3; Indels
57.1%; Pred. No. 2.7e+03;
tive 0; Mismatches 3; Indels
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US-10-767-701-40084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: MRT4577_113213C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(183)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(187)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1"
"--nes 4; Conservative
Best Local Similarity 57.1 Matches 4; Conservative
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                                                                                             162 VSTIAEF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 VTAGAEF 163
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                                                          1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
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APPLICANT: LA KOVALICA:
APPLICANT: LA KOVALICA:
APPLICANT: Exountic, David K.
APPLICANT: Exountic, David K.
APPLICANT: David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Broukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERRNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 209
                                                                                           APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 165533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.8%; Score 18; DB 16; Length 201; Best Local Similarity 57.1%; Pred. No. 3e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 209;
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US-10-437-963-121186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_6432C.1.pep
US-10-437-963-165533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 16;
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(201)
OOTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 121186, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
  Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
57.1%;
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Best Local Similarity 57.1%
                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VAAGAEF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 VTGAAĖF 97
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SEQUENCE 21613, Application US/10425115

SENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: CANDIN Nucleic
APPLICANT: APPLICANT: Nucleic
APPLICANT: APPLICANTON: Nucleic
APPLICANT: APPLICANTON: Nucleic
APPLICANT: APPLICANTON: Nucleic
APPLICANT APPLICANTON: Nucleic
CURRENT APPLICANTON: Number 1031228
CURRENT APPLICANTON NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 271613
LENGTH: 199
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Pred. No. 2.9e+03;
0; Mismatches 3; Indels
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57.1%; Pred. No. 3e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: MRT4577_179304C.1.pep
                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIRAY, HISOSHI
APPLICANT: SHIRAY, TADAYOSHI
APPLICANT: SHRAY, TADAYOSHI
APPLICANT: SHRAY, TADAYOSHI
APPLICANT: HATTORI, MASHHRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR PILING DATE: 2001-05-30
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
57.1%;
Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-165533
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US-10-25-115-199685

i Sequence 199685, Application US/10425115

i Sequence 199686, Application US/10425115

i CENERAL INFORMATION:

i APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

i APPLICANT: Zhou, Yihua

i APPLICANT: Cao, Yongwei

i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

i TITLE OF INVENTION: NUMBER: US/10/425,115

i CURRENT FILING DATE: 2003-04-28

i NUMBER OF SEQ ID NOS: 369326

i ENGTH: 220
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US-10-389-566-1581

Sequence 1581, Application US/10389566

Publication No. US20040025202A1

GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C

TITLE OF INVERTION:
CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT PILING DATE: 2003-03-15

PRIOR APPLICATION NUMBER: US 60/365,301

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-26

SOPTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 LENGTH: 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
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Pred. No. 3.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT3847_105623C.1.pep
US-10-424-599-149059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 VGAAAEF 161
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENGINE ENGINE ENGINE SEQ ID NOS: 285684
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 230315
LENGTH: 212
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Sequence 149059, Application US/10424599

Sequence 149059, Application US/10424599

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.8%; Score 18; DB 15; Length 212; Best Local Similarity 57.1%; Pred. No. 3.2e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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US-10-424-599-149058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49999C.1.pep
US-10-424-599-230315
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OTHER INFORMATION: ungure at all Xaa locations
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Best Local Similarity 57.1°
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VSSLAEF 66
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US-10-44-599-262409

US-10-44-599-262409

Sequence 262409, Application US/10424599

Sequence 262409, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Covalic David K

APPLICANT: Cov Yongus

TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 153223 Brants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 262409

LENGTH: 241
                                         Gaps
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Sequence 90.

Publication No. US20050064527A1

Publication No. US20050064527A1

GENERAL INFORMATION:

APPLICANT: Levy, Stuart, et. al.

TITLE OF INVENTION: NIME COMPOSITIONS AND THEIR METHODS OF USE

FILE REFERENCE: PKZ-043

CURRENT FILING DATE: 2004-07-15

PRIOR PAPLICATION NUMBER: US/09/801, S63

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PALENT OF SEQ ID NOS: 98

SOFTWARE: PALENT OF SEQ ID NOS: 98

SEQ ID NO 98

LENGTH: 240

TYPE: PRI

TYPE:
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Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
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81.8%; Score 18; DB 15; Length 241;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
                                     Indels
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US-10-424-599-262409
      Pred. No. 3.5e+03;
0; Mismatches 3;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
Best Local Similarity 57.1 Matches 4; Conservative
                                                                                                                                                                    151 VSSLAEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
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                                                                                                   1 VXXXAEF 7
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US-10-437-963-115265
                                                                                                                                                                                                                                                                                                   JS-10-893-671-98
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROUNT STOU Withua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION PLANTS
TITLE OF INVENTION 12023)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 247828
LENGTH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1597, Application US/10389566
| Publication No. US20040025202A1
| GENERAL INFORMATION:
| APPLICANT: Monsanto Technology, LLC
| APPLICANT: Laurie, Cathy C
| TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
| TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
| FILE REPRENCE: 38-77(52900)D
| CURRENT APPLICATION NUMBER: US/10/389,566
| CURRENT PLING DATE: 2002-03-31
| PRIOR APPLICATION NUMBER: US 60/365,301
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-26
| NUMBER OF SEQ ID NOS: 2459
| SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                            Score 18; DB 15; Length 228;
Pred. No. 3.4e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 15; Length 228; 57.1%; Pred. No. 3.4e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 15; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_65819C.1.pep
                                                                                                                                                                                                   81.8%;
                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                             TYPE: PRT
ORGANISM: Vicia faba
US-10-389-566-1581
                                                                                                                                                                                                                                                                                                                                                                                         41 VEAAAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 VEABAEF 47
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US-10-424-599-247828
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US-10-389-566-1597
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SEQ ID NO 1581
LENGTH: 228
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LENGTH: 228
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RESULT 87

US-10-424-599-274705

Sequence 274705, Application US/10424599

Sequence 274705, Application Wo. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwal

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement

TURENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 274705

LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_9007C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 81.8%; Score 18; DB 15; Best Local Similarity 57.1%; Pred. No. 3.9e+03; Matches 4; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 COURENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 5807
LENGTH: 258
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Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-5807
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: CHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 VATGAEF 52
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Best Local Similarity
Matches 4; Conserv
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US-09-738-626-5807
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APPLICANT: ECOTIA BLOSCIENCES INC.
APPLICANT: ECOTIA BLOSCIENCES INC.
APPLICANT: MCALDine, James
APPLICANT: ACADEMIC, James
APPLICANT: APPLICANT: Bachman, Brian
APPLICANT: Bachman, Brian
APPLICANT: Piraee, Mahmood
ITILE OF INVENTION: PARNESYL DIBENZODIAZEPINONE, PROCESSES FOR ITS PRODUCTION AND ITS
ITILE OF INVENTION: A PHARMACEUTICAL
FILE REFERENCE: 3005-505
CURRENT APPLICATION NUMBER: US.004-01-20
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-08-07
PRIOR FILING DATE: 2003-08-07
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PACENTIN VESSON 60/518,286
FRIOR FILING DATE: 2003-11-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PACENTIN VESSON 60/518,286
FRIOR FILING DATE: 2003-11-10
                                                                                                                                                                                                                              APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (52221) B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 115265
LENGTH: 252
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81.8%; Score 18; DB 16; Length 252;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
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US-10-437-963-115265
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US-10-762-107-46
Sequence 115265, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-762-107-46
; Sequence 46, Application US/10762107
; Publication No. US20050043297A1
; GENERAL INFORMATION:
                                                                                                                                                                                                      Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 VTMSAEF 205
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 4.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         Length 259;
                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_18060C.1.pep
US-10-437-963-114362
                                                                                                                                                                                                                                                                                         81.8%; Score 18; DB 16;
57.1%; Pred. No. 3.9e+03;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65087, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 57.1%;
4; Conservative
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1-
                                                                                                      ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 VSVSAEF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SEQ ID NO 114362
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SOFTWARE: Pateni
SEQ ID NO 65087
LENGTH: 268
                                                                        TYPE: PRT
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US-10-437-963-114362
Sequence 114362, Application US/10437963
Fublication No. US20040123343A1
Fublication No. US20040123343A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Bring
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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US-10-781-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - See File Wrapper or PALM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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Pred. No. 3.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 784
SEQ ID NO 600
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%;
57.1%;
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Best Local Similarity 57.1
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                                                                US-10-781-014-600
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PRIOR FILING DATE: 2001-05-08
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Trawick, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 VGSSAEF 112
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
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US-10-282-122A-72181
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                                                                                                                                                                                                                                               TYPE: PRT
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/201,078
FRIOR FILING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: 60/200,335
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-110-20
FRIOR FILING DATE: 2000-110-20
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2001-12-20
FRIOR FILING DATE: 2001-12-20
FRIOR FILING DATE: 2001-12-20
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-03-03
FRIOR FILING DATE: 2001-03-03
FRIOR FILING DATE: 2001-03-03
FRIOR FILING DATE: 2001-03-03
FRIOR FILING 
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Publication No. US20040087770A1
GENERAL INFORMATION:
APPLICANT: Tang, Ciristoph
TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
FILE REFERENCE: GJE-6436
CURRENT APPLICATION WHOSER: US/10/275,026A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/GB01/02003
                                                                                                                                                                  Sequence 66020, Application US/10282122A Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
41 VASNAEF 47
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Matches 4; Conserv
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                                                                                                                                     US-10-282-122A-66020
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                                                  h Similarity 57.1%; Pred. No. 4.1e+03; 4; Conservative 0; Mismatches 3; Indels
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US-10-236-031B-16
; Sequence 16, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B
; CURRENT FILING DATE: 2002-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR PILING DATE: 2001-09-05
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 271
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PRIOR APPLICATION NUMBER: GB 0011108.8
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 214
SCPTWARE: PatentIn version 3.2
SEQ ID NO 170
LENGTH: 268
                                                                                                                                                                ) ORGANISM: Neisseria meningitidis
US-10-275-026A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Yamamoto, Robert
Forsyth, R.
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09730329-59ed.rapb

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; Sequence 9623, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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US-10-369-493-9623
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US-10-767-701-34443

Sequence 34443, Application US/10767701

Sequence 344443, Application No. US20040172684A1

SENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535) B

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NOS: 63128

LENGTH: 293
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

FRIOR PAPLICATION NUMBER: 60/191,078

FRIOR APPLICATION NUMBER: 60/206,848

FRIOR APPLICATION NUMBER: 60/206,848

FRIOR APPLICATION NUMBER: 60/207,727

FRIOR FILING DATE: 2000-05-26

FRIOR PILING DATE: 2000-05-26

FRIOR PILING DATE: 2000-09-06

FRIOR FILING DATE: 2000-09-06

FRIOR PILING DATE: 2000-09-09

FRIOR FILING DATE: 2000-10-23

FRIOR PILING DATE: 2000-10-23

FRIOR PILING DATE: 2000-11-27

FRIOR PILING DATE: 2000-11-27

FRIOR PILING DATE: 2000-12-22

FRIOR PAPLICATION NUMBER: 60/257,931

FRIOR PILING DATE: 2001-02-26

FRIOR FILING DATE: 2001-02-16

FRIOR FILING DATE: 2001-02-16
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US-10-767-701-34443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 15;
Pred. No. 4.4e+03;
0; Mismatches 3;
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LOCATION: (1)..(293)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 57.1%
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Sorghum bicolor
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| Sequence 1912, 144-1912
| Sequence 1912, 1
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NESULT 100
US-10-282-1204-52547

| Sequence 52247 Application US/10282122A
| Sequence 52247 Application US/10282122A
| Sequence 52247 Application US/10282122A
| Publication No. US20040029129A1
| SEMENAL INFORMATION:
| APPLICANT: Malone, Carry
| APPLICANT: Malone, Carry
| APPLICANT: Malone, Carry
| APPLICANT: Grant
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| APPL
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Pred. No. 4.7e+03;
0; Mismatches 3; Indels
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; ORGANISM: Desulfitobacterium hafniense US-10-369-493-9623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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; TYPE: PRT; ORGANISM: Clostridium botulinum
; ORGANISM: Clostridium botulinum
US-10-282-122A-52547

Query Match
Best Local Similarity 57.1%; Pred: No. 4.88+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7

Qy 1 VXXXAEF 7

Db 115 VATLAEF 121

Search completed: June 13, 2005, 14:18:24
Job time: 112 secs
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n 5.1.6 Compugen Ltd. earch time 24 Seconds (without alignments)	28.063 Million cell updates/secesidues parameters: 283416 aries	icted by chance to ha e of the result being score distribution. Descrip	NADPH-flavin oxido probable regulator hypothetical prote probable regulator probable exported hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote mega-agatoxin III omega-agatoxin
GenCore versic Copyright (c) 1993 - 2005 OM protein - protein search, using sw model Run on: June 13, 2005, 13:36:32 ; S	Title: Perfect score: 22 Sequence: 1 VXXXAEF 7 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283416 seqs, 96216763 residue Total number of hits satisfying chosen parame Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 00% Listing first 300 summaries	** mber of result or equal to th nalysis of the SUM	1         19         86.4         240         2 P6586           2         19         86.4         298         2 C61041           4         19         86.4         298         2 C61041           5         19         86.4         298         2 C61041           6         19         86.4         298         2 C61041           7         19         86.4         186         2 M6165           8         19         86.4         126         2 A7021           9         19         86.4         146         2 T00095           10         19         86.4         126         2 A6149           10         19         86.4         126         2 A713224           10         19         86.4         126         2 D70095           11         18         81.8         76         2 A5125           13         18         81.8         76         2 D5425           14         18         81.8         76         2 C7425           16         18         81.8         122         2 A44420           16         18         81.8         146         2 T06471

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A;Cross-references: UNIPROT:Q9KU15; GB:AE004158; GB:AE003852; NID:g9655156; PIDN:AAF93886 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC0715 A;Map position: 1 C;Superfamily: NADPH-flavin oxidoreductase homolog		RESULT 2 RESULT 2 FB58BS probable regulator yfeU [imported] - Escherichia coli (strain O157:H7, substrain EDL933) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: FB58BS R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L., Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Status: preliminary	A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: SGTO> A; Cross-references: GB:AE005174; NID:g12516806; PIDN:AAG57546.1; GSPDB:GN00145; UWGP:Z36 A; Experimental source: strain 0157:H7, substrain EDL933 C; Genetics: A; Score 19; DB 2; Length 298; Best Local Similarity 57.1%; Pred. No. 34+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0; DD 172 VXTAREF 7 DD 172 VXTAREF 778	RESULT 3 C65017 hypothetical protein b2428 - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Bscherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 C;Accession: C65017 R;Blatcher, R.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12.	A/Accession: C65017 A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: DNA A/Stat
17 77.3 279 2 T41124 17 77.3 281 2 T01445 17 77.3 283 2 A4814 17 77.3 283 2 A90884 17 77.3 288 2 AD0884 17 77.3 298 2 S18990	17 77.3 295 2 C64123 17 77.3 295 2 C64123 17 77.3 296 1 S52750 17 77.3 296 2 H83456 17 77.3 296 2 E83285 17 77.3 299 1 S68863 17 77.3 299 2 A41900 17 77.3 299 2 G90677	17 77.3 299 2 C85528 17 77.3 300 2 H84022 17 77.3 300 2 S15786 17 77.3 304 2 B91113 17 77.3 304 2 E87084 17 77.3 304 2 C65085 17 77.3 304 2 C65085 17 77.3 309 2 E87671 17 77.3 310 2 AI1059 17 77.3 313 2 C95247	7 77.3 313 2 H98111 conserved 7 77.3 314 2 553492 probable 7 77.3 316 2 AF0309 probable 7 77.3 316 2 C88448 probable 7 77.3 316 1 C88448 probable 7 77.3 318 2 AD1709 probable 7 77.3 321 2 E81301 probable 7 77.3 322 1 JC4033 probable 7 77.3 322 1 JC4033 probable 7 77.3 322 1 JC4033 probable 7 77.3 328 2 AC2987 probable 7 77.3 328 2 H83099 probable 7 77.3 329 2 H83099 probable	17 77.3 330 1 B64561 17 77.3 330 2 A71945 17 77.3 330 2 A83828 17 77.3 330 2 T37854 17 77.3 331 2 A60599 17 77.3 332 2 B85588 17 77.3 332 2 C64816	RESULT 1 D82288 NADPH-flavin oxidoreductase VC0715 [imported] - Vibrio cholerae (strain N16961 serogroup C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C; Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R; Heidelberg, J.F.; Eisen, J.A.; Venter, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M. I, R.R.; MMKAlanos, J.J.; Venter, J.C.; Fraser, C.M. A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUD: 20406833; PMID: 10952301 A; Accession: D82288 A; Accession: D82288 A; Molecule type: DNA A; Residues: 1-240 <a href="https://documer.bitch.com/">HEIS</a>

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R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Ge submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic: A;Reference number: Z20992
                                                                                                                                                A;Accession: T31224
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-484 <ROM>
A;Cross-references: UNIPROT: 085932; EMBL:AF079317; NID:g3378261; PID:g3378365; PIDN:AADDCC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: AF0911
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Aitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove, A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein KIAA0470 - human
C;Species: Homo sapiens (man)
C;Daccession: 200095; fa41155
R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res 4, 345-349; 1997
A;Fitle: Characterization of CDNA clones in size-fractionated cDNA libraries from human h.
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A;Cross_references: UNIPROT:075058; EMBL:AB007939; NID:g3413901; PIDN:BAA32315.1; PID:g3
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A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-1266 APR>
A;Cross-references: GB:AL513382; PIDN:CAD07884.1; PID:g16504431; GSPDB:GN00176
C;Genetics:
A;Gene: STY3549
C;Superfamily: Escherichia coli hypothetical protein yhdP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann,
submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 2; Length 1266;
Pred. No. 1.38+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 2; Dred. No. 4.8e+02; O; Mismatches 3
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                 A,Genome: plasmid pNL1
A,Note: traH
C,Superfamily: traH protein
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                                                                                                     probable regulator [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952 C; Species: Escherichia coli (5.5pecies: Escherichia (5.5pecies: Escherichia (5.5pecies: Escherichia coli (5.5pecies: Escherichia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-298 <HAX>
A;Cross-references: UNIPROT:Q8XBJ2; GB:BA000007; PIDN:BAB36722.1; PID:g13362769; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC81299
C;Superfamily: conserved hypothetical protein b2428
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A;Cross-references: UNIPROT:Q9ZVT5; GB:AE005172; NID:g3850570; PIDN:AAC72110.1; GSPDB:GN
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31224
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C;Superfamily: Arabidopsis thaliana hypothetical protein T419.20
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Pred. No. 3e+02;
0; Mismatches 3; Indels
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les 4, Conservative
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A; Status: preliminary
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C;Accession: A54252
R;Extel, B.A.; Warren, V.A.; Adams, M.B.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108, 1994
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- analy Reference number: A54252; MUID:94227039; PMID:8172884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: D54252
R;Ettel, B.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- and A;Reference number: A54252; WUID:94227039; PMID:8172884
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R; Ertel, B.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M. Biochentry 33, 5098-5108, 1994
A; Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- an A; Reference number: A54252; MUD:94227039; PMID:8172884
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                                                                                                                                                                                                                                                                                                                                             omega-agatoxin III, 8.478K - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Date: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omega-agatoxin III, 8.581K - funnel-weaving spider (Agelenopsis aperta)
C.Species: Agelenopsis aperta
C.Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
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C.Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
        Gaps
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81.8%; Score 18; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
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A;Molecule type: protein
A;Molecule 1-76 < ERT>
A;Experimental source: venom
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: sequence extracted from NCBI backbone (NCBIP:148239)
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Pred. No. 1.5e+02;
0; Mismatches 3;
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Best Local Similarity 57.1%;
Matches 4; Conservative
4; Conservative
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A;Residues: 1-76 <ERT>
A;Experimental source: venom
                                                                                                                                                    1770 VTTSAEF 1776
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                                                                                1 VXXXAEF 7
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A;Residues: 1-1946 <GLA>
A;Cross-references: UNIPROT:092FH4; GB:AL592022; PIDN:CAC95365.1; PID:g16412551; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0132
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A,Residues: 1-2214 <WLL>
A,Cross-references: UNIPROT:Q20219; BMBL:U40420; NID:g1065513; PID:g1065514; PIDN:AAA814
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A;Gene: CESP:F40F4.6
A;Introns: 57/3; 95/1; 302/3; 323/1; 380/1; 404/1; 468/1; 507/2; 547/3; 595/3; 1532/1;
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T16305
T16305
T0505
T16305
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16305
B;Wilson, R:
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F40F4.
A;Reference number: Z18493
A;Reference number: Z18493
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                            A,Accession: T47155
A,Status: preliminary
A;Molecule type: mRNA
A,Residues: 1288-1460 <AAA>
A;Cross-references: EMBL:AL161964
A;Cross-references: Efetal brain; clone DKFZp564B0982
C;Genetion: 1
A;Map position: 1
A;Note: KIAA0470; DKFZp564B0982.1
A; Reference number: Z24374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1425 VSAAAEF 1431
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Query Match

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Rismith, V.

submitted to the EMBL Data Library, September 1994

A;Refecence number: S48407

A;Accession: S48420

A;Molecule type: DNA

A;Residues: 1-121 <SM1>
A;Residues: 1-121 <SM1>
A;Cross_references: UNIPROT:P40520; GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763287; GSi.
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06471
R;Pohlmeyer: K.; Soll, J.; Steinkamp, T.; Wagner, R.
R;Pohlmeyer: K.; Soll, J.; Steinkamp, T.; Wagner, R.
R;Dohlmeyer: Isolation and characterisation of a new type of pore protein present in the A;Reference number: 215701
Proc. Natl. Acad. Sci. U.S.A. 86, 10139-10143, 1989
Affitle: Isolation, partial amino acid sequence, and immunohistochemical localization of
A;Reference number: A34520; MUID:90099311; PMID:2602362
A;Accession: A34520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YIL059c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48420
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                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-92 - WNIN-
A;Cross-references: UNIPROT:P20658
C;Superfamily: calretinin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF hand; vitamin
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-146 <-POH>
A;Cross-references: UDIROT:Q41050; EMBL:Z73553; PIDN:CAA97910.1
A;Experimental source: cv. Golf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 2; Length 121; 57.1%; Pred. No. 2.5e+02; Live 0; Mismatches 3; Indels
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81.8%; Score 18; DB 2; Length 92;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
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C;Superfamily: Saccharomyces probable membrane protein YIL059c
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: MIPS:YIL059c
A;Cross-references: SGD:S0001321
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Best Local Similarity 57.1
Matches 4; Conservative
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CS4252
Omega-gatoxin III, 8.607K - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C54252
R;Etcl; E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108, 1994
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L-A;Reference number: A54252; MUID:94227039; PMID:8172884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-agatoxin IIIA - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Species: Agelenopsis aperta
C;Bacession: A42335
R;Venema, V.J.; Swiderek, K.M.; Lee, T.D.; Hathaway, G.M.; Adams, M.E.
J; Biol. Chem. 267, 2610-2615, 1992
A;Fitle: Antagonism of synaptosomal calcium channels by subtypes of omega-agatoxins.
A;Reference number: A42335; MUID:92129351; PMID:1310319
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calcium-binding protein, vitamin D-dependent - guinea pig (fragments)
C.Species: Cavia porcellus (guinea pig)
C.Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C.Accesaion: A.4520
R;Winsky, L.; Nakata, H.; Martin, B.M.; Jacobowitz, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                     81.8%; Score 18; DB 2; Length 76;
57.1%; Pred. No. 1.5e+02;
tive 0; Mismatches 3; Indels
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A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148241)
  A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148240)
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A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:78693)
                                                                                                               Best Local Similarity 57.1 Matches 4; Conservative
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A Molecule type: protein
A, Residues: 1-76 < ERT>
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Best Local Similarity
Matches 4; Conserva
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-76 <VEN>
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                                                                                          Query Match
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Length 159;

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A;Cross-references: UNIPROT:Q9A714; GB:AE005673; NID:g13423365; PIDN:AAK23887.1; GSPDB:GN C;Genetics: A;Gene: CC1912 C;Superfamily: (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
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A; Residues: 1-190 < ELL>
A; Cross-references: University of the control 
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R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21558
A;Accession: T34819
A;Accession: T34819
A;Keatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-194 <OLI>
A;Residues: 1-194 <OLI
A;Residue
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87486
A;Statuus: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <STO>
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AyTitle: Design and specificity of hammerhead ribozymes against calretinin mRNA.
A;Reference number: 841476; MUID:94077721; PMID:8255773
A;Accession: 841476
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S41476; S34391
R;Ellis, J.; Rogers, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length 155
Pred. No. 3.3e+02;
0; Mismatches 3; Indels
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Similarity 57.1%; Pred. No. 3.9e+02;
4; Conservative 0; Mismatches 3;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Vng1907h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84341
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Acces 10-180486
C;Acces 10-180486
R;Nicerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9HNXO; GB:AE004437; NID:g10581349; PIDN:AAG20100.1; GSPDB:G
C;Genetics:
A;Gene: VNG1907H
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A;Molecule type: DNA
A;Residues: 1-148 esTO>
A;Cross-references: UNIPROT: Q9CE23; GB:AE005176; PID:g12725073; PIDN:AAK06123.1; GSPDB:GA;Experimental source: strain IL1403
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C87486
hypothetical protein CC1912 [imported] - Caulobacter crescentus
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Pred. No. 3e+02;
0; Mismatches
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A,Gene: dpsA
C,Superfamily: hypothetical protein H11349
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                         135 IATAAEF 141
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Matches 4; Conser
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                                                                  VXXXAEF
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A,Status: preliminary
A,Molecule type: DNA
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C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell.
Nature 403, 665-668, 2000
A.Fille: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypela. Reference number: A81250; WUID:20150912; PMID:10688204
A.Reference number: A81250; MUID:20150912; PMID:10688204
A.Reference number: A81250; MUID:20150912; PMID:10688204
A.Reference number: A81250; MUID:20150912; PMID:10688204
A.Residues: 1-212 < PAR>
A.Residues
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2004
C;Accesion: E917174
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos.
A;Reference number: A96900; MUID:21359325; PMID:21359325
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C;Superfamily: Conserved hypothetical protein with haloacid dehalogenase-like hydrolase <
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C;Species: Pisum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 12-Jul-2004
C;Accession: 865425
Bur. J. Biochem. 237, 373-382, 1996
A;Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino acic A;Reference number: 865423; MUID:96215432; PMID:8647075
A;Stetus: preliminary
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A;Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 4.3e+02;
1; Mismatches 3; Indels
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C,Superfamily: thiamin pyrophosphate-binding domain homology
C,Keywords: carbon-carbon lyase; carboxy-lyase
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42.9%;
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Best Local Similarity 42.9
Matches 3; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-213 < KUR>
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A;Residues: 1-228 <MUE>
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R;Acchem. J. 310, 383-387, 1995
Biochem. J. 310, 383-387, 1995
Biochem. J. 310, 383-387, 1995
A;Title: Evolutionary conservation of the vertebrate Ah (dioxin) receptor: amplification A;Accession: 150543; MUID:95382748; PMID:7654172
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C;Species: Campylobacter jejuni
C;Species: Janar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81344
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
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C;Genetics:
A;Gene: AHR2
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A;Residues: 20-211 cHAW>
A;Cross-references: EMBL:X68050; NID:g20021; PIDN:CAA48187.1; PID:g20022
C;Superfamily: ribosomal protein S6, eukaryotic type
C;Keywords: phosphoprotein; protein biosynthesis; ribosome
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A;Molecule type: mRNA
A;Residues: 1-212 <HAH>
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Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                                          58 VSITAEF
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A; Molecule type: mRNA
                                                                          VXXXAEF
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A/Cross-references: UNIPROT: P17117; EMBL: U18655; NID:g609323; PIDN:AAC43450.1; PID:g60932

A/Cross-references: Univert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: C64823

A/Accession: C64824

A/Accession: C64827

A/Accession: GABOOLSY, GB:U00006; NID:g1787070; PIDN:AAC73938.1; PID:g1787075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 134-154,'CA',157,'AGH',161-186,'RHWRSMTSNWRNITSPVAAIIAGIPGAIISAEQSLKKAAHLFWI]
A;Cross-references: GB:X15859; NID:g42745; PIDN:CAA33867.1; PID:g42746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90745
G;Accession: C90745
B;Hayashi, T; Makino, K; Ohnishi, M; Kurokawa, K; Ishii, K; Yokoyama, K; Han, C.G., gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Attle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon A;Accession: C90745
A;Accession: C90745
A;Status: preliminary
A;Residues: 1-240 -HAYs.
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C;Genetics:
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k;Cnatterjee, P.K.; Sternberg, N.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8950-8954, 1995
A;Title: A general genetic approach in Escherichia coli for determining the mechanism(s)
A;Reference number: I59418; WUID:96004656; PMID:7568050
A;Accession: I80318
A;Eccession: I80318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain K-12, substrain MGI655
K; Kang, W.K.; Icho, T.; Isono, S.; Kitakawa, M.; Isono, K.
Mol. Gen. Genet. 217, 281-288, 1989
A; Title: Characterization of the gene rimK responsible for the addition of glutamic acid A; Reference number: S04774; MUID:89364710; PMID:2570347
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57.1%; Pred. No. 4.9e+02;
                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-240 <RES>
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C;Superfamily: NADPH-flavin oxidoreductase homolog
C;Keywords: flavoprotein; FMN; oxidoreductase
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Similarity 57.1%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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G. Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
G. Accession: AGGOS
R. Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, N.S.; Moule, S.; G. Gaoza, P.
Naturners: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: ABOSO2; WUID:21534947; PMID:11677608
A; Residues: preliminary
A; Residues: 1-240 cPAR.
                                                                                                                                                                                                                                                                             pyruvate decarboxylase (EC 4.1.1.1) - fava bean (fragment)
C.Species: Vicia faba (fava bean)
C.Species: Vicia faba (fava bean)
C.Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 12-Jul-2004
C.Accession: 865426
B.;Muecke, U.; Wohlfarth, T.; Fiedler, U.; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S.
Br. J. Biochem. 237, 313-382, 1996
A.Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino aci
A,Reference number: 865423; MUD:96215432; PMID:8647075
A,Residuel type: mRNA
A,Residues: 1-28 e/MUE>
A,Residues: 1-28 e/MUE>
A,Residues: 1-28 e/MUE>
A,Cross-references: UNIPROT:Q7M228
C,Superfamily: thiamin pyrophosphate-binding domain homology
C,Keywords: carbon-carbon lyase; carboxy-lyase
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N;Contains: aromatic nitrate reductase (NADPH) (EC 1.6.6.-) oxygen-insensitive
C;Specias: Escherichia coli
C;Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 180318; C64823; S04774
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Pred. No. 4.7e+02;
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57.1%;
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Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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A;Cross-references: GB:D14615; NID:g287412; PIDN:BAA03466.1; PID:g287413
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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R; Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; El
J. Gen. Virol. 74, 1709-1713, 1993
A; Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the All
A; Reference number: PQ0651; MUID:93346985; PMID:8393919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: P00661
A;Molecule type: mRNA
A;Resdues: 1-247 <NAK.
A;Cross-references: GB:D14622; NID:g287426; PIDN:BAA03473.1; PID:g287427
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14616; NID:g287414; PIDN:BAA03467.1; PID:g287415
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: human rotavirus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                Query Match 81.8%; Score 18; DB 2; Length 247 Best Local Similarity 57.1%; Pred. No. 5.1e+02; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                   C,Genetics:
A,Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C, Keywords: hemagglutinin; outer capsid protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Residues: 1-247 <NAK>
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A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14621; NID:g287424; PIDN:BAA03472.1; PID:g287425
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
                                                                                                           C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: G85595
E;Potecession: G85595
E;Potecession: G85595
E;Potecession: G85595
A;Riber, L; Grotbeck, E.J; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Itle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: DNA
A;Residues: 1-240 <STO>
A;Residues: 1-240 <STO>
A;Coss-references: UNIPROT:Q8X681; GB:AE005174; NID:g12513866; PIDN:AAG55227.1; GSPDB:Q
A;Exomental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: mdaA
C;Superfamily: NADPH-flavin oxidoreductase homolog
                                                                                   modulator of drug activity A [imported] - Escherichia coli (etrain 0157:H7, substrain Ed
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PQ0662
outer capsid spike protein VP4 - feline rotavirus A (strain Cat2) (fragment)
NiAlternate names: VP8* protein
C;Species: feline rotavirus A
C;Species: feline rotavirus A
C;Species: feline rotavirus A
C;Accession: PQ0662
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J, Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
A;Reference number: PQ0651; MUID:93346985; PMID:8393919
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A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A;Accession: PQ0651; MUID:93346985; PMID:8393919
A;Accession: PQ0652
A;Molecule type: mRNA
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C;Superfamily: rotavirus outer layer protein VP3
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A, Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the Al A; Reference number: PQ0651; MUID:93346985; PMID:8393919
A, Accession: PQ0660
A, POlecule + VP29: mRNA
A, Polecule + VP29: mRNA
A, Residues: 1-247 < NAK.>
A; Residues: 1-247 < NAK.>
C; Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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NyAlternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Date: human rotavirus
C;Date: human rotavirus
C;Date: human rotavirus
C;Accession: PQ0659
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; F.
J. Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the Al A;Reference number: PQ0651; MUID:93346985; PMID:8393919
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KRebidues: 1-247 cNAK.
A;Cross-references: GB:D14623; NID:9287428; PIDN:BAA03474.1; PID:9287429
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemagg
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A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the Al A;Reference number: PQ0651; MUID:93346985; PMID:8393919
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C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Molecule type: mRNA
A; Residues: 1-247 <NAK>
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PQ0656
Outer capsid spike protein VP4 - human rotavirus (strain AU387) (fragment)
NyAlternate names: VP8* protein
NyAlternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Species: human rotavirus
C;Bote: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0656
R;Makagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
A;Reternee number: PQ0651; MUID:93346985; PMID:83393919
A;Accession: PQ0656
A;Molecule type: mRNA
A;Residuse: 1-474 cNNA
A;Residuse: 1-474 cNNA
A;Residuse: 1-474 cNNA
A;Residuse: 1-474 cNNA
A;Residuse: 1-247 cNNA
A;Coss-references: GB:DJ4617; NID:g287416; PIDN:BAA03468.1; PID:g287417
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
                                                                                                                           Problem 199

Outer capsid spike protein VP4 - human rotavirus (strain AU115) (fragment)

Noter capsid spike protein

C;Species: human rotavirus

C;Species: human rotavirus

C;Date: 14-Unl-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000

R;Naccession: 0.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993

A;Title: Nuclectide sequence comparison of the VP8* gene of rotaviruses possessing the A;Accession: PQ0651

A;Accession: PQ0651

A;Accession: PQ0651

A;Accession: PQ0651

A;Residues: 1-247 <ANAX>

A;Cross-references: GB:D14613; NID:g287408; PIDN:BAA03464.1; PID:g287409

A;Cross-references: GB:D14613; NID:g287408; PIDN:BAA03464.1; PID:g287409

C;Coment: This protein plays a role in viral neutralization, viral virulence and haemag
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PO0660
Outer appid spike protein VP4 - human rotavirus (strain PCP5) (fragment)
N.Alternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Accession: PQ0660
C;Accession: PQ0660
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
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57.1%; Pred. No. 5.1e+02;
tive 0; Mismatches 3; Indels
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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Best Local Similarity 57.1%
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Matches 4; Conservative
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N'Alternate names: VP-8 protein
C;Species: human rotavirus A
A;Variety: isolate 5193
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
C;Accession: S61221
R;Gollop, R.; Kaga, E.; Silberstein, I.; Shulman, L.; Nakagomi, O.; Mendelson, E.; Shif, submitted to the EMBL Data Library, August 1995
A;Description: Three forms of AU-1 like viruses differentiated by their overall genomic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q86509; EMBL:X90733; NID:g967070; PIDN:CAA62267.1; PID:g96707
A,Experimental source: strain AU-1; isolate 5193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Cross-references: UNIPROT:Q86512; EMBL:X90736; NID:g967076; PIDN:CAA62270.1; PID:g9670°
Experimental source: strain AU-1; isolate 6460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer capsid spike protein VP-8 - human rotavirus A (isolate 6460 and others) (fragment) N;Alternate names: VP-8 protein
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                                                                                outer capsid spike protein VP-8 - human rotavirus A (isolate 5193) (fragment)
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A,Experimental source: strain AU-1; isolate 6584
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A;Experimental source: strain AU-1; isolate 7044
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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81.8%; Score 18; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: VP-8
C,Superfamily: rotavirus outer layer protein VP3
C,Keywords: outer capsid protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A;Accession: S61221
A;Molecule type: genomic RNA
A;Residues: 1-247 <GOL>
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Molecule type: genomic RNA
Residues: 1-247 <GOW>
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Molecule type: genomic RNA
Residues: 1-247 <GOF>
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A; Residues: 1-247 <GOA>
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                                                                                                                                                                                                                                                             Outer capsid spike protein VP4 - human rotavirus (strain AU125) (fragment)

N.Alternate names: VP8* protein
C.Speciale: human rotavirus
C.Speciale: human rotavirus
C.Speciale: human rotavirus
C.Jacte: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C.Accession: PQ0653
R.Accession: PQ0653
A.Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A.Reference number: PQ0651; MUID:93346985; PMID:8393919
A.Reference number: PQ0651; MUID:93346985; PMID:8393919
A.Residues: 1-247 cARA.
A.Residues: 1-247 cARA.
A.Residues: 1-247 cARA.
A.Residues: This protein plays a role in viral neutralization, viral virulence and haemag C.Gennetics:
A.Gene: VP4
C.Superfamily: rotavirus outer layer protein VP3
C.Reywords: hemagglutinin; outer capsid protein
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A;Residues: 1-247 <NAK2>
A;Cross-references: GB:D14618; NID:g287418; PIDN:BAA03469.1; PID:g287419
A;Experimental source: strain AU720
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
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NyAlternate names: VP9* protein
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0657; PQ0654
R;Nakagomi, O:; Isegawa, Y:; Ueda, S:; Gerna, G:; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J;Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
R;Reference number: PQ0651; MUID:93346985; PMID:8393919
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A;Experimental source: strain AU785
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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     Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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C,Superfamily: rotavirus outer layer protein VP3
C,Keywords: hemagglutinin; outer capsid protein
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57.1%;
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Similarity 57.1%;
4; Conservative (
57.1%;
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Best Local Similarity 57.1%
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                              4; Conservative
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     Best Local Similarity
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A; Residues: 1-247 <NAK1>
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Best Local Similarity
Matches 4; Conserv
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                              Matches
                                                                                                                                                                                                                      RESULT 43
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C.Species: Serratia marcescens
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
S,Viejo, M.; Enfedaque, J.; Regue, M.
R,Viejo, M.; Enfedaque, J.; Regue, M.
A,Reference number: S34724
A,Reference number: S34724
A,Reference number: S34724
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-254 <VIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q54472; EMBL:Z25281; NID:g395948; PIDN:CAA80898.1; PID:g39594 (S.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology C;Keywords: oxidoreductase (P;7-190/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 27-Oct-2003
C,Accession: 140886
K;Chlumsky, L.J.; Zhang, L.; Jorns, M.S.
J. Biol. Chem. 270, 1825-18259, 1995
A;Title: Sequence analysis of sarcosine oxidase and nearby genes reveals homologies with A,Reference number: A57385, MUID:95355441; PMID:7543100
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69337
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
F;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Karchum, K.A.; Dodson
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.?
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycine hydroxymethyltransferase (EC 2.1.2.1) - Corynebacterium sp. (fragment) N.Alternate names: serine aldolase; serine hydroxymethylase; threonine aldolase C;Species: Corynebacterium sp.
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A;Cross-references: EMBL:U23955; NID:g927587; PIDN:AAC43458.1; PID:g927588
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C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;60/Binding site: pyridoxal phosphate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length 254;
Pred. No. 5.2e+02;
0; Mismatches 3; Indels
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                                                                                      robable oxidoreductase (EC 1.1.1.-) - Serratia marcescens
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                 RESULT 49
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                                                                                                                                                                                        RESULT 48

5374373
heat shock protein grpE - Synechocystis sp. (strain PCC 6803)
N/Alternate names: hypothetical protein sll0057
C;Species: Synechocystis sp.
G;Avriety: PCC 6803
C;Accession: S74373
Requence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74373
Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, W.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A,Molecule type: genomic RNA
A,Rosidues: 1-247 - GGON-
A,Fossi-references: EMBL:X90735; NID:g967074; PIDN:CAA62269.1; PID:g967075
A,Experimental source: strain AU-1; isolate 5960
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <KAN>
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A;Gene: VP-8
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: outer capsid protein
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A.Gene: grpE
C.Superfamily: heat shock protein grpE
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Matches 4; Conservative
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                                                       199 VSSDAEF 205
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Matches 4; Conserv
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VXXXAEF 7
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histidine-binding periplasmic protein NWA1811 [imported] - Neisseria meningitidis (strair C,Species: Neisseria meningitidis (strair C,Species: Neisseria meningitidis (c)Species: Neisseria meningitidis (c)Species: Neisseria meningitidis (c)Species: Nava-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 (c)Accession: H81806 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell Mature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: H81806 A;Accession
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A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Verl A; Accession: B81063
A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Accession: B81063
A; Scatus: preliminary
A; Scatus: preliminary
A; Residues: 1.268 < TET>
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A;Experimental source: serogroup B, strain MC58
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: OS-May-2000 #sequence_revision OS-May-2000 #text_change O9-Jul-2004
CiAccession: S14109; A60253
RiParmentier, M.; Lefort, A.
Bur. J. Blochem. 196, 79-88, 1991
A;Title: Structure of the human brain calcium-binding protein calretinin and its express)
A;Reference number: S14109; MUID:91160569; PMID:2001709
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81063
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C;Superfamily: lysine-arginine-ornithine-binding protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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$550699
cordidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia ohmeri)
C;Species: Pichia ohmeri
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #te
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A;Rebidues: 1-261 cPIR>
A;Cross-references: UNIPROT:P48844; EMBL:Z35100; NID:g510926; PIDN:CAA84483.1; PID:g5109
A;Note: the source was formerly designated as Pichia ohmeri
                                                                                                                                                                                              A;Reaidues: Î-260 «KLE»
A;Cross-references: UNIPROT:029556; GB:AE001056; GB:AE000782; NID:g2689379; PIDN:AAB9053
C;Superfamily: thiamin biosynthesis protein thil
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*Residues: 1-268 c.LAV-
A,Cross-references: UNIPROT:Q06758; EMBL:X64421; NID:g49067; PIDN:CAA45768.1; PID:g49068
C;Superfamily: lysine-arginine-ornithine-binding protein
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C;Keywords: carbon-carbon lyase; carboxy-lyase; pyrimidine nucleotide biosynthesis
F;1-261/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>
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C;Species: Neisseria gonorrhoeae
C;Species: Oc-Jan-1995 #sequence_revision O6-Jan-1995 #text_change O9-Jul-2004
C;Accession: S19184
R;Lavitola, A.; Vanni, M.; Martin, M.V.; Bruni, C.B.
submitted to the EMBL Data Library, January 1992
A;Description: Cloning and characterization of a Neisseria gene homologous to hisJ and A;Accession: S19184
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                                                    A;Accession: F69337
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A; Reference number: A69250; MUID: 98049343; PMID: 9389475
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4; Conservative
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chloramphenicol resistance protein BH2116 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C:Species: Bacillus halodurans C;Date: 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:O9KB19; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BABO58:
A;Experimental source: strain C-125
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 5.9e+02;
0; Mismatches 3;
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C;Superfamily: probable transcription regulator lsyR
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                                                                                               106 VGSSAEF 112
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A,Molecule type: DNA
A,Residues: 1-293 <STO>
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1 VXXXAEF
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A; Molecule type: protein
A; Molecule type: pro
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525006
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus Norsequence_revision 05-May-2000 #text_change 09-Jul-2004
CiDate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
CiSpecies: Nature Norsequence of rat calretinin cDNA: Evolutionary conservation of AiDescription: Nucleoide sequence of rat calretinin cDNA: Evolutionary conservation of
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A; Residues: 1-271 <STR>
A; Residues: 1-271 <STR>
A; Cross-references: UNTROT: P47728; EMBL: X66974; NID: 955852; PIDN: CAA47385.1; PID: 955853
R; Gabrielides, C.; McCormack, A.L.; Hunt, D.F.; Christakos, S.
Biochemistry 30, 656-662, 1991
A; Title: Brain calbindin-D-28k and an M-r 29 000 calcium binding protein in cerebellum a
A; Reference number: A38396; MUID: 91105154; PMID: 1988053
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Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Filor-139/Domain: calmodulin repeat homology <EF3>
Filor-183/Domain: calmodulin repeat homology <EF4>
Filor-227/Domain: calmodulin repeat homology <EF5>
Filor-227/Domain: calmodulin repeat homology <EF5>
Filor-22,14,126,131/Binding site: calcium (Asp, Asp, File4,166,168,170,175/Binding site: calcium (Asp, Asp, Filor-212,214,219/Binding site: calcium (Asp, Asp, Filor-212,214,219/Binding site: calcium (Asp, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 16q22.2-16q22.2
C;Superfamily: calretinin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF h:
F;16-48/Domain: calmodulin repeat homology <EF1>
F;63-95/Domain: calmodulin repeat homology <EF2>
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F;151-183/Domain: calmodulin repeat homology <EF4>
F;195-227/Domain: calmodulin repeat homology <EF5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 81.8%; Score 18; Similarity 57.1%; Pred. No. 54; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB:125374; OMIM:114051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S25006
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                                                                                                     A; Molecule type: DNA
A; Residues: 1-271 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-271 <PA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:CALB2; CAL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A60253
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C.)Accession: A84304

R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. F.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablori Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A.)Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; List A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:Q9HPSO; GB:AE004437; NID:g10580993; PIDN:AAG19797.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah: awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kinda, Res. 6, 83-101, 1999
A;Fitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-320 <KAW>
A;Residues: 1-320 <KAW>
A;Cross-references: UNIRKOT:Q9YE96; DDEJ:AP000060; NID:g5104188; PIDN:BAA79650.1; PID:dl(.
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0677
                                                                                                                                                                                                                                                                                                                                         hypothetical protein Vng1497c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable prephenate dehydratase - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Feb-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72656
         Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 317;
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Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein APE0677 - Aeropyrum pernix (strain K1)
   Score 18; DB 2; Le
Pred. No. 6.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; I
Pred. No. 6.5e+02;
0; Mismatches 3;
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 81.8%;
Similarity 57.1%;
4; Conservative
      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 VTHAAEF 179
                                                                                                                                                                                        268 VTTRAEF 274
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
                                                                                                                                1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: A84304
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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H69312
conserved hypothetical protein AP0504 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10.58p-1999 #sequence_revision 10.58p-1999 #text_change 09-Jul-2004
C;Accession: H69312
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, E.
Naturnors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Retaus: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9ZUH5; GB:AE002093; NID:g4115379; PIDN:AAD03380.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-301 <KLE>
A;Cross-references: UNIPROT:029746; GB:AE001069; GB:AE000782; NID:g2689392; PIDN:AAB9073
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1629
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NiAlternate names: protein T31P16.220
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cibate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
CiAccession: T50027
RiBevan, M.; Zimermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohldmann, P.; submitted to the Protein Sequence Database, May 2000
A; Reference number: 225027
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Nature 402, 761-768, 1999
Aritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Fitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84633
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
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A,Gene: ATSP:T31P16.220
A,Map position: 5
A,Introns: 26/1; 74/3; 147/3
C,Superfamily: annexin I; annexin repeat homology
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A, Cross-references: UNIPROT: Q9LX07;
                                                                                                                                                                                                                                                                                                                                                                        81.8%;
                                                                                                                                                                                                                                                                                                                                         274 VESAAEF 280
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A; Status: preliminary
A; Molecule type: DNA
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A,Map position: 2
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A.Molecule type: DNA'
A.Residues: 1-333 <GUS>
A.Cross-references: UNIPROT:Q59500; GB:L49392; NID:g1196506; PIDN:AAB38428.1; PID:g11965(
C.Genetics:
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C,Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hon
C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F,18-200/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Accession: A69059
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E; Smith, D.R.; Spadafora, R.; Vicaire, R.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
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A;Cross-references: UNIPROT:027491; GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAB8591:
A;Experimental source: strain Delta H
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C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hon
F;25-207/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CjAccession: UC5166
R;Gusberti, L.; Cantoni, R.; De Rossi, B.; Branzoni, M.; Riccardi, G.
Gene 177, 83-85, 1996
A;Title: Cloning and sequencing of the ilvBNC gene cluster from Mycobacterium avium. A;Reference number: JC5164; MUID:97080504; PMID:8921849
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A;Molecule type: DNA
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          A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5H1.06c
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                Score 18; DB 2; Le:
Pred. No. 6.7e+02;
0; Mismatches 3;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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[Species: Mycobacterium leprae
[Species: Wycobacterium lep
C; Accession: C70653

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A; Authors Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Reference number: A70500; MUD: 98295987; PMID: 9634230

A; Reference number: A70500; MUD: 98295987; PMID: 9634230

A; Residual preliminary; nucleic acid sequence not shown; translation not shown

A; Residuals: 1-31 c.COL>

A; Residuals: 1-31 c.COL>

A; Residuals GB: 283864; GB: AL123456; NID: 93261687; PIDN: CAB06203.1; PID: 91781119
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A;Cross-references: GB:AL450380; NID:g13092467; PIDN:CAC29586.1; GSPDB:GN00147
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C,Superfamily: prephenate dehydratase; prephenate dehydratase homology
F;2-284/Domain: prephenate dehydratase homology <PPW>
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C;Superfamily: prephenate dehydratase; prephenate dehydratase homology
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Query Match 81.8%; Score 18; DB 2; Length 321; Best Local Similarity 57.1%; Pred. No. 6.6e+02; Matches 4; Conservative 0; Mismatches 3; Indels

C, Genetics:

216 VAALAEF 222

1 VXXXAEF 7

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A;Cross-references: UNIPROT:Q9X7R4; EMBL:AL049863; PIDN:CAB42931.1; GSPDB:GN00070; SCOED
hypothetical protein SC5H1.06c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: O5-Nov-1999 #sequence_revision O5-Nov-1999 #text_change O9-Jul-2004 C;Accession: T3532 R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Rioliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A;Accession: T3532 A;Accession: T353
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Query Match 81.8%; Score 18; DB 2; Length 322; Best Local Similarity 57.1%; Pred. No. 6.6e+02; Matches 4; Conservative 0; Mismatches 3; Indels

A;Accession: F86918 A;Status: preliminary A;Molecule type: DNA

C, Genetics

218 VAALAEF 224

RESULT 67

1 VXXXAEF 7

09730329-59ed.rpr

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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95103
R;Tettelin, H:; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heide On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIRROT:Q97RC6; GB:AE005672; PIDN:AAK75023.1; PID:g14972371; GSPDB:GNA;Experimental source: strain TIGR4
C;Genetics:
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C;Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinase
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RiHoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Esle, Y.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McI, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001

Ajuthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MuID:21429245; PMID:11544234

A;Status: preliminary

A;Residues: 1-335 <WUR>
A;Residues: 1-335 <WUR
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C;Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinase
C;Keywords: phosphotransferase
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R;Keilhauer, C.; Eggeling, L.; Sahm, H.
J. Bacteriol. 175, 5595-5603, 1993
A;Tile: Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ill
A;Reference number: A48648; MUID:93374855; PMID:8366043
A;Accession: C48648
A;Status: preliminary
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C;Genetics:
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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C;Species: Corynebacterium glutamicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 6.9e+02;
0; Mismatches 3; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70855
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: D70855
A;Accession: D70855
A;Status: proliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-333 <COL>
A;Cross-references: UNIPROT:053248; GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CAA1608
A;Experimental source: strain H37RV
                                                                                                                                                                                                                                             Retol-acid reductoisomerase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Spacession: H87120
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
N.A.; Davies, R.M.
N.A.; Steutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Accession: H87120
A;Accession: H87120
A;Accession: H87120
A;Accession: Preliminary
A;Retsidues: 1-333 <STO>
A;Residues: 1-333 <STO>
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C;Genetics:
A;Gene: ilvC
C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hq
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A,Gene: ilvC
C,Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hc
F;18-200/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Species: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; L
Pred. No. 6.9e+02;
0; Mismatches 3;
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57.1%;
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                                                                 255 VSNTAEF 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
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VXXXAEF
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C;Accession: B87463
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT: Q9A7J7; GB:AE005673; NID:g13423142; PIDN:AAK23702.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein VC1791 [imported] - Vibrio cholerae (strain N16961 serogr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-346 <HEL>
A,Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:g9656310; PIDN:AAF9494
A,Experimental source: serogroup O1; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CiSpecies: Escherichia coli (strain K CiSpecies: Escherichia coli (strain K CiSpecies: Escherichia coli (cispecies: Escherichia coli (cispecies: Escherichia coli (cispecies: Escherichia coli (cispecies: Escherichia) (cispeciesion: Escherichia coli (cispeciesion: FS131) (cispeciesion: FS131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
                                                             hypothetical protein CC1726 [imported] - Caulobacter crescentus
C,Species: Caulobacter crescentus
C,Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: C82156
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Pred. No. 7.1e+02;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAEAAĖF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
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A,Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved hypothetical protein AF0507 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69313
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback C.R.; Venter, J.C.
A;Altile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69313
A;Accession: C69313
A;Accession: C69313
A;Accession: C40313
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A;Residues: 1-342 <KLE>
A;Access-references: UNIPROT:029743; GB:AE001069; GB:AE000782; NID:g2689392; PIDN:AAB9073
                         A;Cross-references: UNIPROT:057179; GB:L09232; NID:9551777; PIDN:AAA62431.1; PID:9400336 C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase F:22-204/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd
F;28-210/Domain: ketol-acid reductoisomerase homology <KAR>
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Cibate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000
Cibate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000
Cibate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000
Cibates: T45415
A;Reference number: 216918
A;Reference number: 216918
A;Status: T45415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-343 <PAR>
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                                                                                                                                                                                                        Score 18; DB 1; Length 338;
Pred. No. 76+02;
0; Mismatches 3; Indels
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Similarity 57.1%; Pred. No. 7e+02;
4; Conservative 0; Mismatches 3; Indels
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T45415
ketol-acid reductoisomerase (imported) - Mycobacterium leprae
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A;Experimental source: cosmid B637
                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            252 VSDTAEF 258
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Matches 4; Conserv
A;Residues: 1-338 <KEI>
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hypothetical protein PA2209 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yhfN
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-347 < shift>
A;Cross-references: GB:AE000413; GB:U00096; NID:g2367215; PIDN:AAC76396.1; PID:g1789772;
C;Genetics: C;Genetics: strain K-12, substrain MG1655
A;Gene: yhfN
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Best Local Similarity 42.9.
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140 ITSAAEF 146
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-347 <STO>
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phosphoserine aminotransferase homolog serC (imported) - Listeria monocytogenes (strain E
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Glaser, P.; Farini, H.,
J; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A, Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matlok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Molecule type: DNA
A;Residues: 1-35 acid.A
A;Cross=references: UNIRROT:Q8Y3L0; GB:NC_003210; PIDN:CAD01038.1; PID:g16412325; GSPDB:C
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mailok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession. AF1801
A;Accessio
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                                                              C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Accession: AF1801
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0; Mismatches 3;
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C;Superfamily: phosphoserine aminotransferase
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C;Superfamily: phosphoserine aminotransferase
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Best Local Similarity 57.1%;
Matches 4; Conservative
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C; Accession: H83369

09730329-59ed.rpr

C; Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12

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A; Experimental source: strain MSB8
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42.9%;
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Best Local Similarity 42.9%;
Matches 3; Conservative
                                                       Query Match 81.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 3; Conservative
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A;Molecule type: DNA
A;Residues: 1-392 <KUR>
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E95261
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: H8336
A;Accession: H8336
A;Accession: H8369
A;Accession: H8368
A;Accession: 
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A;Molecule type: DNA
A;Molecule types: DNA
A;Residues: 1-368 <STO>
A;Kesidues: 1-368 <STO>
A;Cross-references: UNIPROT:Q9K611; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB076
A;Experimental source: strain C-125
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Cross-references: UNIPROT:P91984; EMBL:Z81050; PIDN:CAB02859.1; GSPDB:GN00023; CESP:C5
A;Experimental source: clone C50B6
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D84140
citrate synthase III mmgD [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
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C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C'Accession: T20093
R'Percy, C.
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A;Introns: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 2; I
57.1%; Pred. No. 7.5e+02;
iive 0; Mismatches 3;
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A;Reference number: 21922
A;Accession: T20093
A;Accession: T20093
A;Btatus: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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57.1%;
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C,Superfamily: Citrate synthase
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A;Gene: CESP:C50B6.10
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A, Gene: PA2209
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maltose ABC transporter, periplasmic maltose-binding protein - Thermotoga marítima (stran C; Species: Thermotoga marítima C; Species: Il-Jun-1999 #sequence_revision Il-Jun-1999 #text_change 09-Jul-2004 C; Accession: B72283 #sequence_revision Il-Jun-1999 #text_change 09-Jul-2004 C; Accession: B72283 #sequence_revision Il-Jun-1999 #text_change 09-Jul-2004 B.H.; Hickey, R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ. A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: 09X0T1; GB: AE001777; GB: AE000512; NID: 94981751; PIDN: AAD36279
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A,Experimental source: Clostridium acetobutylicum ATCC624
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Pred. No. 8.1e+02;
1; Mismatches 3; Indels
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Pred. No. 8.1e+02;
1; Mismatches 3; Indels
Score 18; DB 2; Length 371
Pred. No. 7.6e+02;
0; Mismatches 3; Indels
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A;Gene: pdc
C;Superfamily: thiamin pyrophosphate-binding domain homology
         A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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G84200
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serine proteinase [imported] - Streptococcus pneumoniae (strain TIGR4)

(;Species: Streptococcus pneumoniae

C;Date: 03-Wug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: B95261

R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt. I.B.
Science 293, 498-506, 2001

A;Authors: Loftud, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                       A,Accession: E95261
A,Status: preliminary
A,Status: Draliminary
A,Residuse: 1-393 «KUR»
A,Cross-references: UNIPROT:Q97N37; GB:AE005672; PIDN:AAK76286.1; PID:g14973750; GSPDB:G
A,Experimental source: strain TIGR4
C,Generics:
A,Gene: SP2239
C,Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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C;Species: Halobacterium sp. NRC-1
C;Species: Ralobacterium sp. NRC-1
C;Accession: C84394
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID: 20504483; PMID: 11016950
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CiSpecies: Streptococcus pneumoniae
CiAccession: B98127
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Ie, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I., P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <STO>
A;Cross-references: UNIPROT:Q9HMQ2; GB:AE004437; NID:g10581841; PIDN:AAG20519.1; GSPDB:
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57.1%; Pred. No. 8.10+02;
tive 0; Mismatches 3; Indels
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A, Gene: argG
C, Superfamily: argininosuccinate synthase
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Matches 4; Conserv
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A;Accession: B98127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Residues: 1-397 <KUR>
A;Cross-references: UNIPROT:O06670; UNIPROT:Q8DMW2; GB:AE007317; PIDN:AAL00847.1; PID:g1:
C;Genetics: sphra
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; trypsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cipace 102-7 Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Cipacession: G84200
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lie A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: G84200
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <STO>
A;Cross-references: UNIPROT:Q9HS37; GB:AE004437; NID:g10580033; PIDN:AAG18971.1; GSPDB:GP
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C;Species: Pisum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 12-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 12-Jul-2004
C;Accession: S65471; S65424
R;Muecke, U; Wohlfarth, T.; Fiedler, U.; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S. Bur. J Blochem. 237, 373-382, 1996
A;Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino acic
A;Reference number: S65423; MUID:96215432; PMID:8647075
A;Accession: S65471
A;Status: mucleic acid sequence not shown
A;Residues: 1-405 «MUE»
A;Accession: S65424
A;Accession: S65424
A;Accession: S65424
A;Accession: S65424
A;Residues: 1-8;146-153;209-218;350-362;386-393 «MUW»
C;Genetics:
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C;Superfamily: Bacillus halodurans cytochrome P450 BH0579; cytochrome
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F;353/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 8.2e+02;
0; Mismatches 3; Indels
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Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome P450 [imported] - Halobacterium sp. NRC-1
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Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endor
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95972
                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: 0926G0; GB: AL5919B5; PIDN: CAC49444.1; PID: g15140930; GSPDB: GRA; Experimental source: strain 1021, megaplasmid pSymB R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 S.A. Alauthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.G. A; Title: The composite genome of the legume symbiont Sinorhizobium mellioti.
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A;Cross-references: UNIPROT:Q66640; GB:U20824; NID:g695172; PIDN:AAC13824.1; PID:g695209
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S6588
A;Title: CDNA cloning of BR-gamma, a novel brain-specific isoform of the B regulatory sul A;Reference number: S65685; MUID:95331316; PMID:7607250
A;Reference number: S65685
A;Reference number: S6
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5631
R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Tetle: The DNA sequence of equine herpesvirus 2.
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57.1%; Pred. No. 8.7e+02;
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C;Species: Rattus sp. (rat)
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les 4; Conservative
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                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
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A;Genome: plasmid
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Matches
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C;Species: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 23-Jun-1993
C;Accession: C38351
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, W Biochemistry 30, 3589-3597, 1991
A;Title: Structure of the 55-kDa regulatory subunit of protein phosphatase 2A: evidence A;Reference number: A38351; MUD:91198016; PMID:1849734
A;Status: preliminary
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D95972
D95972
Cycbable sugar uptake ABC transporter periplasmic solute-binding protein precursor SMb21
C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95972
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
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C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Accession: S57820
R;Bucher, M.; Brander, K.A.; Sbicego, S.; Mandel, T.; Kuhlemeier, C. Plant Mol. Biol. 28, 739-750, 1995
A;Hille: Aerobic fermentation in tobacco pollen.
A;Feference number: S57819; MUID:95375236; PMID:7647304
                                                                                                                                                                                                                                           Gaps
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           C;Keywords: carbon-carbon lyase; carboxy-lyase
F;1-405/Product: pyruvate decarboxylase #status experimental <MAT>
F;271-317/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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Pred. No. 8.3e+02;
0; Mismatches 3; Indels
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A,Status: preliminary; nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-417 - 8UC.
A,Cross-references: EMBJ:X81854
C,Superfamily: thiamin pyrophosphate-binding domain homology
C;Keywords: carbon-carbon lyase; carboxy-lyase
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Pred. No. 8.5e+02;
0; Mismatches 3;
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C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative (
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ilarity 57.1%;
Conservative
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Matches 4; Conservative
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4; Conserve
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A; Residues: 1-412 < MAY>
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C38351
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phosphoprotein phosphatase 2-beta regulatory chain - human
NyAlternate names: phosphoprotein phosphatase 2A-beta 55K regulatory chain B
C;Species: Homo saplens (man)
C;Datesis: Homo saplens (man)
C;Accession: B38351
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, N
Bychemistry 30, 3589-3597, 199
A;Title: Structure of the 55-kDa regulatory subunit of protein phosphatase 2A: evidence
A;Reference number: A38351; MUD:91198016; PMID:1849734
A;Accession: B38351
A;Status: preliminary
A;Residues: 1-443 <mAX>
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Misphosphotein phosphatase 2-alpha regulatory chain - human
MyAlternate names: phosphoprotein phosphatase 2A-alpha 55K regulatory chain B
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38351
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, W
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, W
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, W
R;Mayer, R.S.; Hendrix, P.; MuD:91198016; PMID:1849734
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A;Residues: 1-447 <MAY>
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A;Gente: GDB:PPP2R2B
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Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL, ABC16942. AAC78999.1; ...
Complete proteome; Hypothetical protein.
SEQUENCE 116 AA; 11869 MW; DFAC729A3C3B9FAC CRC64;
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PubMed=12444438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Ilijima M., Ikeda M., Ikeno M., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
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Sukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
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Giardia lamblīa ATCC 50803.
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                                                                                                 h Similarity 57.1%; Pred. No. 1e+03; Length 116; 4; Conservative 0; Mismatches 3; Indels
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SEQUENCE 126 AA; 13845 MW; 2BE6EEB9F73D7D7D CRC64;
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmicheel L.K.,
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Q94em8
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P51845
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Bacteroidaceae; Bacteroides.
                                                           28×844
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Last annotation update)
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Q67NZ8
TOBAC
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Q6UVS4
O06670
Q8DMW2
Q9GSG9
Q8DRQ6
                                                                                                  Q9ZP53
Q9SOP5
Q94EWB
Q94EMB
Q6ABX6
SERC_LISIN
SERC_LISMO
                                           Q9KR55
FRLB ECO57
Q6MN<u>Y</u>3
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2ABB_RABIT
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P91984
Q8NLP4
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Q6D4S8
Q6MMF4
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Q83B80
Q7PJ50
Q8FLY3
Q9H6P6
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Q97DG9
Q97N37
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Q7W717
Q7WIS4
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Q911Q8
Q9CWU3
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(TrEMBLrel. 24, L
(TrEMBLrel. 24, L
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OrderedLocusNames=BT3794;
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01-JUN-2003
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    Q8A172
Q8A172;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                         Hypothetical protein DKFZp564B0982.
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium diphtheriae.
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 VSAAAEF 144
                                                                          Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                                                                              NCBI_TaxID=9606;
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Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV060702; AAL28260.1; -
FlyBase; FBGN0037525, CG17816.
SEQUENCE 159 AA; 17663 MW; C33175B9B3436C4D CRC64;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                          "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
BMBL; AP004369; BAB90783.1; --
HSSP; O82040; 1K9U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 19; DB 2; Length 146; 57.1%; Pred. No. 1.3e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%; Score 19; DB 2; Length 159; 57.1%; Pred. No. 1.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00018; EF HAND; 3.
Calcium; Calcium-binding.
SEQUENCE 146 AA; 16257 MW; C6DDE4C8612A2E7C CRC64;
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Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                              Gramene, OBRXJB; -.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF Hand like.
Prom; PF00036; Efhand; 3.
ProDom; PD000012; EF-hand; 2.
SWART; SM00054; EFh; 4.
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nes 4; Conservative
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Q9NSN9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95SM3;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
GH14459p.
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Matches
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AC 095SM3
AC 095SM3
AC 01-D
DT 01-D
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Q9NSN9
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Nucleic Acids Res. 31:6516-6523(2003).
Nucleic Acids Res. 31:6516-6523(2003).
-!- SIMILARITY: Contains 1 HTH tetR-type DNA-binding domain.
EMBL; BX248356; CAE49362.1; --
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009057; HTH_TetR.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bictype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Parlen M.J. Bentley S.D., Bestration A., Dower L.G., Holdem M.T.G., De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., Hamlin N., Holroyd S., Jagels K., Monle S., Quail M.A., Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitchead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                       TISSUE=Brain;
Poustka A., Wellenreuther R., Mewes H.W., Weil B., Wiemann S.;
Submitred (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Alltd19481291; -.
Hypothetical protein.
SEQUENCE 173 AA; 19157 MW; E3CEF034CIE5D4BB CRC64;
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1717;
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Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 2; Length 173; Pred. No. 1.5e+03; 0; Mismatches 3; Indels
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SEQUENCE 222 AA; 24446 MW; 14DD3E055EBC79F1 CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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GO; GO:0007242; P:intracellular signaling cascade; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clavispora lusitaniae.
                                                                                                                                                                                                                                 201 VATAAEF 207
                                                                                                                                                                                                     1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK repeat
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                                                                                                                                                                                                                                                                                                       Q691P2
                                                                                                       Kinase
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     SERBERBBR
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Submitted (MAK-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AKI31548; BAD18682.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINEL TOR NIG961 / Serotype Ol;
MEDLINE=20406833, Pubmed=10952301, DOI=10.1038/35020000;
Meldelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                      Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.; "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 19; DB 2; Length 240; 57.1%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA; 26500 MW; F856E48C3BD6980E CRC64;
                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000415; Nitroreductase.
                   240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00881; Nitroreductase; 1.
                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483 (2000).
EMBL; AE004158; AAF93880.1; -.
PIR; D82288; D82288.
HSSP; Q56691; 1BKJ.
TIGR; VC0715; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein FLJ16784.
Homo sapiens (Human).
                                                                                     NADPH-flavin oxidoreductase.
                                                                                                    OrderedLocusNames=VC0715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                 PRELIMINARY;
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Best Local Similarity
4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 VASAAEF 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                 Vibrio cholerae
                                                                                                                                                           NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                cholerae.
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                Q9KU15
Q9KU15;
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Gaps
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Metschnikowiaceae; Clavispora.
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Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
"Oryza sativan on propher,"
submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, APRO6753; BAD3219.1; -.
InterPro; IPR002119, ANK.
Pfam; PP00023; Ank; 4.
                                                                                                                                                                                                                          Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.4%; Score 19; DB 2; Length 255; 57.1%; Pred. No. 2.1e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                       SEQUENCE 243 AA; 27566 MW; 23D41825EB9F782D CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TremBrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        Query Match 86.4%; Score 19; DB 2; Best Local Similarity 57.1%; Pred. No. 2e+03; Matches 4; Conservative 0; Mismatches
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InterPro; IPR008973; C2 CalB.
InterPro; IPR002219; DAG_PE-bind.
Pfam; PF00130; C1 1; 1.
PRINTS; PR00109; DAGPEDOWAIN.
SWART; SM00109; C1; 1.
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PROSITE; PS50297; ANK REP REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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258 VSAAAEF 264
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Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                     1 VXXXAEF
                                                                                                                                 39 VTTTÄEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Q8XBJ2;
                                                                                                                                                                                                                                                                     Q96L14;
                                                                                                                                                                                                                                              096L14
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YFEU_ECO57
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MEDLINE=98117054; PubMed=9457876;
MEDLINE=98117054; PubMed=9457876;
MEDLINE=98117054; PubMed=9457876;
Manayama N., Ueda M., Atomi H., Tanaka A.;
"Genetic evaluation of physiological functions of thiolase isozymes in the n-alkane-assimilating yeast, Candida tropicalis.";
J. Bacteriol. 180:690-698 (1998).
-I- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
-I- PATHWAY: Pyrimidine biosynthesis.
-I- SIMILARITY: Belongs to the OMP decarboxylase family.
EMBL; AB006207;
                                                                                                                                                                                                                                                           -I- PATHMAY: Pyrimidine biosynthesis.
-I- SIMILARITY: Belongs to the OMP decarboxylase family.
BMBL, AF450297; AAL47842.1; -.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0004590; F:orotidine-5'-phosphate decarboxylase activity; IEA.
GO; GO:0006207; P:'de novo' pyrimidine base biosynthesis; IEA.
PF00215; OMPdecase; 1.
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GO:0004590; F:orotidine-5'-phosphate decarboxylase activity; IEA.
GO:0006207; P:'de novo' pyrimidine base biosynthesis; IEA.
GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
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                  Francois F., Chapeland-Leclerc F., Villard J., Noel T.; "Development of an integrative transformation system for the opportunistic pathogenic yeast Candida lusitaniae using URA3 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                           STRAIN=CBS 6936;
Francois-Vadrot F., Chapeland-Leclerc F., Villard J., Noel T.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 2; Lengtn 2007. Pred. No. 2.2e+03;
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SEQUENCE 267 AA; 29521 MW; 48D2C8CBFP85846B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Decarboxylase, Lyase, Pyrimidine biosynthesis.
SEQUENCE 264 AA, 28913 MW, 98949F050BBEB79B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23).
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InterPro; IPR011060; RibP bind barrel.
Pfam; PF00215; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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TIGREAMS; TIGR01740; DyrF; 1.
PROSITE; PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMB; TIGR01740; pyrF; 1.
PROSITE; PS00156; OMPDECASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                            (east 21:95-106(2004).
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  STRAIN-CBS 6936;
                                                                                       selection marker
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042694;
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042694
AC 04269
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DT 01-JU
DT 0
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RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.P., Zeeberg B. Buetow K.H., Schmeen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schmeer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buetow K.H., Schmeer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R. Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R. Brownstein M.J., Widna T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.R., Gunzaratne P.H.,
R. Hidton D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Schwichenko Y., Boulfard G.G.,
Whiting M., Madan A., Young A.C., Schwichenko Y., Boulfard G.G.,
Mithing M., Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Chriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
R. Generation and initial analysis of more than 15,000 full-length human
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                                                     Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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     Length 267;
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Pred. No. 2.48+03;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014590; AAH14590.2; -.
Hypothetical protein.
SEQUENCE 293 AA; 32648 MW; 74904E44B67399F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
Score 19; DB 2; Le:
Pred. No. 2.2e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein yfeU.
Name-yfeU; OrderedLocusNames=z3693, ECs3299;
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                     293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 AA.
                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                     PRT;
     86.4%;
                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 101-MR-2004 (TrEMBLrel. 26, 101-MR-2004 (TrEMBLrel. 26, 14) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57...
4, Conservative
                                                        4; Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Name=yfeU; OrderedLocusNames=b2428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO0274; GCKR like; 1.
PROSITE; PS01272; GCKR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; ME_00068; -; 1.
InterPro; IPR005486; GCKR.
InterPro; IPR005488; GCKR_like.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016764; AAN81411.1; -.
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 VSSTAEF 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
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YFEU ECOLI
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:14 / Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7 "; Nature 409:529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                    STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., MayNew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Agodteck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0157:H7 and genomic comparison with a laboratory strain K-12.";
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298 AA; 31112 MW; 231B33A48F7E1E81 CRC64;
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57.1%; Pred. No. 2.5e+03;
tive 0; Mismatches 3;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 8:11-22(2001).
-!- SIMILARITY: Belongs to the GCKR family.
-!- SIMILARITY: Contains 1 SIS domain.
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Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF01380; SIS; 1.
TIGRFAMB; TIGR00274; GCKR like; 1.
PROSITE; PS01272; GCKR; 1.
                   Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00068; -; 1.
InterPro; IPR005486; GCKR.
InterPro; IPR005488; GCKR_like.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005473; AAG57546.1; -. EMBL; AP002561; BAB36722.1; -.
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                                                                        SEQUENCE FROM N.A.
                                 NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein yfeU.
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QRFFE0;
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Matches
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SEQUENCE FROM N.A.
STRAIN=06.H1 / CFT073 / ATCC 700928 / UDEC;
MEDLINE=23388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
MEDLINE=23388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
MEDLINE=23388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
Mayhew G.F., Bullind V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-i. SIMILARITY: Belongs to the GCKR family.
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MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN 56 214 SIS.
SEQUENCE 298 AA; 31105 MW; 3F6DECAE3F784994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P76535; P76965; P76966; P76967;
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
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Bordetella pertussis.
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                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
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                                                                                        [3]
IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE=99420866; PubMed=10493127.
DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELES2181>3.3.CO;2-H;
Pountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of Iow abundance proteins of Escherichia coli by
"Enrichment of Iow abundance proteins of Escherichia coli by
hydroxyapatite chromatography."
Electrophoresis 20:2181-2195(1999).
-- SIMILARITY: Baclongs to the GCKR family.
-- SIMILARITY: Contains 1 SIS GCKR family.
--- SIMILARITY: Contains 1 SIS GCKR family.
--- CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 87.
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takhahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamaqata S., Horiuchi T.; "Construction of a contiguous 874-kb sequence of the Escherichia coli-K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Shigella flaxmeri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%; Score 19; DB 1; Length 298; 57.1%; Pred. No. 2.5e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 214 SIS.
298 AA; 31220 MW; 34FBBFB78EBB3077 CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein yfeU.
Name=yfeU; OrderedLocusNames=SF2481, S2629;
                                                                                                                                                                                                                                                                                                                                                                          EMBL, U00096; AAC75481.1; -.
EMBL, D90872; BAA16311.1; ALT_FRAME.
EMBL, D90872; BAA16312.1; ALT_FRAME.
EMBL, D90873; BAA16312.1; ALT_FRAME.
EMBL, D90873; EAA16315.1; -.
ELOBASE; EB3914; -.
ECOGGOG, EG14162; YfeU.
HAMAP; MF 00068; -; 1.
INTERPO: IPR005488; GCKR.
INTERPO: IPR005488; GCKR.
INTERPO: IPR005488; GCKR.
INTERPO: IPR005488; GCKR.
INTERPO: IPR00548; GCKR.
INTERPMS: TIGR00274; GCKR.
FF01380; SIS; I.
TIGRPMS: TIGR00274; GCKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 57.1
es 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 VSTTAEF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
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MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
                                                                                                                                                                   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella flexmari serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
-! SIMILARITY: Belongs to the GCKR family.
-! SIMILARITY: Contains 1 SIS domain.
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Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
DOI=10.1128/INA.171.5.2775-2786.2003;
Wei J. Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
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31183 MW; FB63F15725C1091F CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-ORT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BP0330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 AA.
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InterPro; IPR005486; GCKR.
InterPro; IPR001347; SIS.
InterPro; IPR001347; SIS.
Pfam; PP01380; SIS.
TIGRFAMS; TIGR0274; GCKR.like; 1.
PROSITE; PS01272; GCKR, 1.
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"Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).
EMBL; AR0171331.1; -.
Hypothetical protein.
SEQUENCE 379 AA; 44618 MW; F3D59CE9A9F47F6E CRC64;
                                                                                                                                                                                               Digital Total Bole 10.1038/nbt959; Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Rolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Lambda integrase-like, N-terminal, DNA breaking-
rejoining enzyme, catalytic core)
ORFNAmes-BL01373, BLi01428;
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                                                                       Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
NCBI_TaxID=882;
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                                                  Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 377;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR011053; Hybrid motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE017309; AAS94609.1; -. TIGR; DVU0125; -.
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                              OrderedLocusNames=DVU0125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 377 AA;
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EMBL, AY268839; AAQ11668.1; -.

GO, GO:0008171; F:O-methyltransferase activity; IEA.

GO, GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.

GO, GO:0016740; F:transferase activity; IEA.

InterPro; IPR001601; Methyltransf.

InterPro; IPR009051; SAM bind.

InterPro; IRR009058; Wing ha.

Methyltransferase; Transferase.

SEQUENCE 355 AA; 39842 MM; DD408079B18D8F71 CRC64;
                                                                                                                                                                                 Nat. Genet. 35:32-40(2003).
BMBL; BX640411; CAE40707.1; -.
GO: GO:000288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
InterPro; IPR005064; UPP0065.
Chillingworth T., Collins M., Cronin A., Davis P., Boggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norbersak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares R., Green S., Stevens K., Unwin L., Whitchead S., Barrell B.G., Waskell D.J., "Comparative analysis of the genome sequences of Borderella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Papaver somniferum (Opium poppy).
Bakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; Ranunculales, Papaveraceae; Papaver.
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                                                                                                                                                                                                                                                                                                                                                              Length 338;
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                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEQUENCE 338 AA; 34618 MW; 65F3D103502CE118 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 2.8e+03;
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                    Pfam; PF03401; Bug; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 VAASAEF 293
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Best Local Similarity
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Plant J. 36:808-81
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Q6WUC2

RESULT 18

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Matches

RESULT 19 Q72FT8 ID Q72FT AC Q72FT DT 05-JU DT 05-JU

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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hookawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh Y., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
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Sukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vysotekala V.S., Schwartz J.R., Toriumi M., Yu G., Li J., Liu S., Kremenetskala I., Luros J., Araujo R., Buehler E., Conway A.B., Dewer K., Feng J., Kim C., Li Y., Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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                                       86.4%; Score 19; DB 2; Length 379; 57.1%; Pred. No. 3.1e+03; ive 0; Mismatches 3; Indels
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SEQUENCE 385 AA; 44026 MW; 37D15C4701304A0A CRC64;
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Last annotation update)
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, C;
01-DEC-2001 (TrEMBLrel. 19, Ls
01-OCT-2002 (TrEMBLrel. 22, Ls
P0583G08.7 protein.
Name=P0583G08.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24,
Query Match
Best Local Similarity 5/...
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 57.1
nes 4; Conservative
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                                                                                                                                                                                                                                                                                                45 VAAAAEF 51
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094217
AC 094217
AC 094217
DT 01-DE 01-DE DT 01-OC OC Sperm OC Sp
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Q9ZVTS
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MEDLINE=22423060; PubMed=12534463;
Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H.,, Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., Yano M., Jiang J., Gojobori T., "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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0
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TIGR; PED16793; AAN70827.1; --
                                                                                                                                                                                                           INTERPRO; IPRO04314; DUF239.
Pfam; PF03080; DUF239; 1.
SEQUENCE 435 AA; 47559 WW; 49CB0F59D6B46DF5 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-QCT-2003 (TrEMBLrel. 25, Last annotation update)
MATE efflux family protein.
OrderedLocusNames=PP5262;
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GO; GO:0015297; F:antiporter activity; IEA.
GO; GO:0015238; F:drug transporter activity; IEA.
GO; GO:0006855; P:multidrug transport; IEA.
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01-NOV-1998 (TrEMBLrel. 08, Created)
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NCBI_TaxID=160488;
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TIGRFAMS; TIGR00797; matE; 1.
                                                                                                                                                  EMBL; AP003282; BAB64772.1;
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Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
genomic perspective.";
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STRAIN=HDL00 / DSM 50701 / ATCC 15356 / NCIB 9529;
STRAIN=HDL00 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 303:689-692(2004).

EMBL, BX842649; CAE79080.1; -.

GO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0003779; F:actin binding; IEA.

GO; GO:000710; P:actin binding; IEA.

InterPro; IPR002097; Profilin.
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                                                                                                                                                                                                                                                                Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                 Vibrio vulnificus.

Barceria; Porceobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.4%; Score 19; DB 2; Length 516; Best Local Similarity 57.1%; Pred. No. 4.1e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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Pred. No. 4.16+03;
                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ARD16800; AAO09608.1; -.
Complete proteome.
SEQUENCE 516 AA; 57283 MW; 1DC881279BD2C1EF CRC64:
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                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Microtubule binding protein.
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                            Created)
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                        01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26, efficted membrane protein. OrderedLocusNames=VVIII34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bdellovibrio bacteriovorus.
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Best Local Similarity 57.1
Matches 4; Conservative
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SEQUENCE 522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=959;
                                                                                                                                                                                                                                                           STRAIN=CMCP6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14656965; DOI=10.1101/gr.1295503; Chang C.-H., Tsai H.-C., Chang C.-H., Tsai H.-C., Mux., Wu K.-M., Chen H.-J., Shen A.B.-T., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; "Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C., Sensen C., Gaasterland T., Fredrickson J.K., Saffer J.D.; "Complete sequence of a 184-kilobase catabolic plasmid from Sphingomonas aromaticivorans F199-"; J. Bacteriol. 181:158-vrans F199-"; J. Bacteriol. 181:158-vrans F199-"; PRD: 731224; T31224. InterPro; IPR010927; TraH. Plasmid; Signal.
                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium.
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VIBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 2; Length 484;
Pred. No. 3.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 2; Length 516;
Pred. No. 4.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 516 AA; 57208 MW; 5626021DC1B521A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 AA; 52034 MW; 992DC004E93C4C40 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Pilus assembly and synthesis protein precursor.
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Last annotation update)
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                                                                                                                                                                                                                                                       MEDLINE=99175459; PubMed=10049392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13:2577-2587(2003).
EMBL; AP005330; BAC92857.1; -.
                                                                                       Sphingomonas aromaticivorans.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicted membrane protein. OrderedLocusNames=VV0093;
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                                                                                                                                                                                                                                   STRAIN=F199;
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                                                                   Name=traH;
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RESULT 25 Q7MQB5

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RESULT 26 Q8DD76 ID Q8DD76

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STRAIN=CLIB99;
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                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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STRAIN=JCM 10545 / 7;
STRAIN=JCM 10545 / 7;
MEDLINE=214565165, PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044201; AAH44201.1; -.
ZFIN; ZDB-GENE-030131-9382; zgc:55619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 575 AA; 66162 MW; A3EDACD583A73531 CRC64;
             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein zgc:55619.
ORFNames=zgc:55619;
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Last annotation update)
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STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 0
01-DEC-2001 (TrEMBLrel. 19, 1
01-MAR-2004 (TrEMBLrel. 26, 1
Hypothetical protein ST2017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences."
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchher C., Cauddron B., Scarpelli C., Gaillardin C., Weissenbach J.,
"Genome evolution in yeasts.";
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Mauda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Saccharomycetales; Dipodascaceae; Yarrowia.
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 2; Length 599;
Pred. No. 4.7e+03;
0; Mismatches 3; Indels
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                                                                                                                      "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          EMBL; AP000988; BAB67116.1; -.
InterPro; IPR011013; Gal mut. Like.
InterPro; IPR010918; Glyco trans. 6hp.
InterPro; IPR010916; TONB Box N.
PROSITE; PS00430; TONB DEFENEBRIT REC.1; UNKNOWN. 1.
CCMplete proteome; Hypothetical protein.
SEQUENCE 599 AA; 69660 NW; P8B94CAE7731D119 CRC64;
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InterPro; IPR007244; MAXLO_Actrans.
Pfam; PF04112; MaXLO; 1.
SEQUENCE 712 AA; 79869 MW; 4E5D512544154E11 CRC64;
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57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipolytica.
ORFNames=YALIOF08591g;
Yarrowia lipolytica CLIB99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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Best Local Similarity
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"Pacifastin, a novel 155-kDa heterodimeric proteinase inhibitor containing a unique transferrin chain.";
Proc. Natl. Acad. Sci. U.S.A. 94:6682-6687(1997).
- I- FUNCTION: Transferring are iron binding transport proteins which bind ferric iron in association with the binding of an anion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00455; Transferrin; 2.
PRINTS; PR0422; TRANSFERRIN.
SMAAL; SM00094; TR FER; TR FER; TR FER; PR05256; TRANSFERRIN 2; 1.
Iron transport; Metal-binding Signal; Transport.
1 22 Potential.
1 22 Potential.
SEQUENCE 977 AA; 106866 MW; 5EF1706133350E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP005946; BAC48398.1; -. GO; GO:0016874; F:ligase activity; IEA. GO; GO:0016779; F:nucleotidyltransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IFR005190; GINE. Pfam; PF03710; GINE.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glutamate-ammonia-ligase adenylyltransferase.
Name-glufs, OrderedLocusNames=blrili3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 AA.
                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006879; P:iron ion homeostasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001156; Peptidase_S60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 VSAAAEF 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-USDA110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 33
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-1 - SURCELLULAR LOCATION: Cytoplasmic (By similarity).
-1 - SIMILARITY: Belongs to the GPI family.
-1 - SIMILARITY: Belongs and the GPI family.
-1 - SIMILARITY: Belongs and the GPI family.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: IEA.
-1 - SIMILARITY: Belongs and the GPI family: FRONG and the GPI fa
                                                                                                                                                                                                                                                                                                                                                                                                            Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconobacter.
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MEDLINE=97338078; PubMed=9192625; DOI=10.1073/pnas.94.13.6682;
Liang Z., Sottrup-Jensen L., Aspan A., Hall M., Soderhall K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Sugiyama M., Suzuki S., Tonouchi N., Yokozeki K.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transaldolase and glucose-6-phosphate isomerase bifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.4%; Score 19; DB 2; Length 957; 57.1%; Pred. No. 7.2e+03; ive 0; Mismatches 3; Indels
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TIGREPANS, PRODES, GEPISOMERASE.
TIGREPANS, TREGUOSTS, tal mycobact; 1.
PROSITE; PS01054; TRANSALDOLASE_1; 1.
Gluconeogenesis; Glycolysis; Isomerase.
SEQUENCE 957 AA; 103122 WW, ISS07DF271E11B07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977 AA.
                                                                                                                                                                                957 AA.
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les 4; Conservative
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                              300 VTSSAEP 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate.
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                                                                                                                                                                                                         Q76EM6;
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P91775
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MEDLINE=22484999; PubMed=12597275; Kanako T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.; Gaps "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002). usually bicarbonate (By similarity).
-!- DOMAIN: Composed of two homologous domains (By similarity).
-!- SIMILARIY: Belongs to the transferrin family.
EMBL; US1824; AAC64660.1; -.
HSSP; P56410; IAOV. ö ö Complete proteome; Ligase; Nucleotidyltransferase; Transferase. SEQUENCE 995 AA; 110118 MW; DCF10D729E67A533 CRC64; Bradyřhizobium japonicum. Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium. 86.4%; Score 19; DB 2; Length 977; 57.1%; Pred. No. 7.4e+03; tive 0; Mismatches 3; Indels Query Match 86.4%; Score 19; DB 2; Length 995; Best Local Similarity 57.1%; Pred. No. 7.5e+03; Matches 4; Conservative 0; Mismatches 3; Indels

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1 VXXXAEF 7
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                                              Best Local Similarity
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  ANK repeat.
                                    Query Match
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Q92K44
                                                          Matches
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-!- SUBCELLUAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

EMBL; AE017201; AAS08381.1; --
GO: 0000986; C.cell surface; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              86.4%; Score 19; DB 2; Length 1096; 57.1%; Pred. No. 8.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLP 375 36878 33303.
Giardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                          Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                        1096 AA; 114350 MW; 4C8A938FB8FAC284 CRC64;
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001899; Gram pos anchor.
Pfam; PF00746; Gram pos anchor; 1.
TRGRAMS; TIGR01167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM POS ANCHORING; 1.
Cell wall; Complete proteome; Hypothetical protein;
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Last sequence update)
Last annotation update)
                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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InterPro; IPR00110; ANK.
Pfam; PF00023; Ank; 9.
PRINTS; PR01415; ANK/REN.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                 Created)
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                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                               OrderedLocusNames=LJ0391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            Peptidoglycan-anchor.
SEQUENCE 1096 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
 816 VSASAEF 822
                                                                                                                  Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 VSTSAĖF 295
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=33959;
                                                                                                                                                                                                              STRAIN=NCC 533;
PubMed=14966310;
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                                 RESULT 34
Q74L34
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Q7QTJ4
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                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21396507; PubMed=11481430; DOI=10.1073/pnas.161294398; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Ranard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analygis of the chromosome sequence of the legume symbiont Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

BMBL, ALS91789; CAC46716.1; BMBL, ALS91789; CAC46716.1; Complete protecome; Hypothetical protein. SEQUENCE 1234 AA; 130531 MW; 772A245CD29F56IC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Pred. No. 9.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                       Score 19; DB 2; Length 1191;
Pred. No. 8.8e+03;
1191 AA; 132435 MW; 70A77664DD550A2D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SMc01454.
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Last annotation update)
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                                                                                                                     0; Mismatches
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                                                       h 86.4%;
Similarity 57.1%;
4; Conservative
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Similarity 57.1%;
4; Conservative
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
Possible exported protein.
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                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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DOI=10.1128/JB.185.7.2330-2337.2003,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparity genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
J. Bacteriol. 185:2330-2337(2003).
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TISSUB-Brain;
MEDLINE-99116662; PubMed-9455484;
Seki N., Ohira M., Nagage T., Ishikawa K., Miyajima N., Nakajima D.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Length 1266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1460;
                                                                                                                                                                                     Score 19; DB 2; Length 126
Pred. No. 9.4e+03;
0; Mismatches 3; Indels
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AB022659; BAA89380.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR00253; FHA.
FAND FFAN.
SMART; SM00240; FHA; 1.
SMART; RM00240; FHA; 1.
SMART; BS0006; FHA; 1.
SCOURNE 1460 AA; 161436 MW; BAD23EBCA19B65F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 2; Length 146
Pred. No. 1.1e+04;
0; Mismatches 3; Indels
                                                                                                                                EMBL; AE016845; AA070819.1; -.
SEQUENCE 1266 AA; 138744 MW; 339C4A88D35922B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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   MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                                                       86.4%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Name=KIAA0470;
Homo sapiens (Human).
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                                                                                                                                                                                                          Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                         895 VSSSAEF 901
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                                                                                                                                                                                                                                                                   1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=kab;
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Q7LGA9;
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Q7LGA9
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MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

MCDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

MCDLILland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                              Gaps
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Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Mitchead S., Barrell B.G.,
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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Enterobacteriaceae, Salmonella.
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Enterobacteriaceae, Salmonella.
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                                                                                                                                                                       Length 1266;
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                                                                        Nature 413:848-852(2001).
EMBL, AL621218, CAD07884.1; -.
COMDLETE FORCEOME.
SEQUENCE 1266 AA, 138661 MW, ECEA91FE03086C91 CRC64;
                                                                                                                                                                   Score 19; DB 2; Length 126
Pred. No. 9.4e+03;
0; Mismatches 3; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=yhdP; OrderedLocusNames=STM3369;
Salmonella typhimurium.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 57.1.,
Best Local Similarity 57.1.,
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STRAIN=Ty2 / ATCC 700931;
                                                                                                                                                                                                          Conservative
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                                                                                                                                               Query Match
Best Local Similarity
Local 4; Conserv?
                                                                                                                                                                                                                                                                                     895 VSSSAEF 901
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EMBL; AB022657; BAA83378.1; -.
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    "Characterization of cDNA clones in size-fractionated cDNA libraries
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR008984; SMAD_FHA.
InterPro; IPR00498; FHA; 1.
Pram; PR00498; FHA; 1.
PROSITE; PS50006; FHA, DOMAIN; 1.
SEQUENCE 1486 AA; 164568 MW; 79312F1C5CB9D04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1472 AA; 162839 MW; 81C2CDC135B45093 CRC64;
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Hara Y., Adachi Y.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
KARP-1-binding protein 2 (KAB2).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
KARP-1-binding protein 1 (KAB1).
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                                from human brain.";
DNA Res. 4:345-349(1997).
EMBL; AB007939; BA432315.2; -.
FIR; T00095; T00095.
InterPro; IPR009594; SMAD_FHA.
InterPro; IPR009594; SMAD_FHA.
SMART; SM00240; FHA; 1.
PROSITE; PSS0006; FHA, 10.
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Best Local Similarity 57.1.
A; Conservative
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Matches 4; Conservative
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090008
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STRAIN=CLIP 11562 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;

A Glaser P., Frangeul L., Buchtrisser C., Rusniok C., Amend A.,

A Glaser P., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Grariff A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

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B Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goobel W., Gomez-Lopez N., Haif T., Hauf U., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Jones L.-M., Schlueter T., Simoes N., Tierrez A.,

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Romer B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Nordsiek G., Novella S.,

Comparative genomics of Listeria species.";

Science 294:849-852(2001).

B RBL, AL596163; CAC95365.1; -.

PIR, AE149; AE1449.

B InterPro; IPR003961; FN III.

SMART; SM00060; FN3; 1.

Complete proteome.

SQUENCE 1946 AA, 215361 MW; DAIB4B630F9B62B3 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                 Query Match 86.4%; Score 19; DB 2; Length 1584; Best Local Similarity 57.1%; Pred. No. 1.2e+04; Matches 4; Conservative 0; Mismatches 3; Indels
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Interpro; IPR000253; FHA.
Interpro; IPR008984; SMAD_FHA.
Ffam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS0006; FHA DOMAIN; 1.
SEQUENCE 1584 AA; 175321 MW; A99D76ED374531F0 CRC64;
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Pred. No. 1.4e+04;
0; Mismatches 3; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORFNames=YALI0F20724g;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1549 VSAAAÈF 1555
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Gaps
                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: Contains 6 EGF-like domains.
EMBL; U40420; AAA81430.1; -.
EMBL; U40420; AAA81430.1; -.
WORMBase: WGGENEO0018237; F40F4.6.
WormPep; F40F4.6; CE04536.
GO; GO:0005529; F: Sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid F40F4."; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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PROSITE; PS50234; VWFA; 1.
EGF-like domain; Hypothetical protein.
SEQUENCE 2214 AA; 243435 MW; B0B38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRR000042; EGF 2.
InterPro; IRR0000429; EGF 2.
InterPro; IRR0006210; EGF 2.
InterPro; IRR000210; EGF 7.
InterPro; IRR001304; InterPro; IRR001304; InterPro; IRR002035; WF A.
Pfam; PF00008; EGF; I.
Pfam; PF00008; EGF; I.
Pfam; PF00005; VWA; I.
SWART; SW00034; VWA; I.
SWART; SW00181; EGF; 3.
SWART; SW00181; EGF; 3.
SWART; SW00181; EGF; 3.
PROSITE; PS00041; EGF 1; PROSITE; PS00042; EGF 1; PROSITE; PS00042; EGF 1; PROSITE; PS00022; EGF 1; PROSITE; PS00022; EGF 1; EFCTIN-PROSITE; PS00022; EGF 1; EFCTIN-PROSITE; PS00022; EGF 1; EFCTIN-PROSITE; PS00022; EGF 1; EFCTIN-PROSITE; PS01186; EGF 2; 3.
Hypothetical protein F40F4.6.
Name=F40F4.6; ORFNames=F40F4.6;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Matches 4; Conservative
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                                           Caenorhabditis elegans.
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                                                                                                              NCBI_TaxID=6239;
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Q6E7J8
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                                                                                                                                                                 A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
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Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
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A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
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Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Wincker P., Souciet J.L.;
I "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, CR382132, CAG78485.1; -...
GO; GO:0005524; C:nucleus; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000524; F:ATP-dependent helicase activity; IEA.
GO; GO:000167; F:DNA binding; IEA.
GO; GO:000166; F:NNA-directed RNA polymerase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0001668; F:type ICI ele-specific deoxyribonuclease ac. ..; IEA.
GO; GO:0003307; P:DNA restriction; IEA.
GO; GO:0003307; P:DNA restriction; IEA.
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                       Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
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SMART; SM00611; SEC63; 2.
ATP-binding; Helicaee; Hydrolase.
SEQUENCE 2106 AA; 234728 MW; 772389CAFP107619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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Interpro; IPR001410; DEAD.
Interpro; IPR011545; DEAD/DEAH N.
Interpro; IPR001650; Helicase C.
Interpro; IPR006993; ResIII.
Interpro; IPR011260; RNAP alpha_C.
Interpro; IPR01179; Sec63.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
Yarrowia lipolytica CLIB99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF04851; ResIII; T. Pfam; PF02889; Sec63; 2. SMART; SM00382; AAA; 2. SMART; SM0487; DEXDC; 2.
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Matches 4; Conservative
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                                                            NCBI_TaxID=284591;
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                                                                                                          SEQUENCE FROM N.A.
                                                                                                                               STRAIN-CLIB99;
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                                                                                                                                                      Genolevures;
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PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
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TX3A AGEAP
ID TX3A AGEAP
AC P33034;
DT 01-0CT-1993 (
DT 05-JUL-2004 (
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                                                                                                                                                                               "Structure and Blosynthesis of the Jamaicamides, New Mixed Polyketide-Peptide Neurotoxins from the Marine Cyanobacterium Lyngbya majuscula.";
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                                                                          STRAIN=JHB;
PubMed=15217615; DOI=10.1016/j.chembiol.2004.03.030;
Edwards D.J., Marquez B.L., Nogle L.M., McPhail K., Goeger D.E.,
Roberts M.A., Gerwick W.H.;
                                                                                                                                                                                                                                     Chem. Biol. 11:817-833(2004).
-1- COFACTOR: Pyridoxal phosphate (By similarity).
-1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
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                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the group II decarboxylase family
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Pfam; Pro0668; Condensation; 1.
Pfam; Pro0601; Ketcacyl-synt; 1.
Pfam; Pro0502; Pr-binding; 2.
Pfam; Pro0550; Pr-binding; 2.
Pfam; Pro0522; Pyridoxal dec; 1.
PRINTS; PRO0154; AMPBINDING.
PROSITE; PS00015; ACP DOWAIN; 2.
PROSITE; PS00012; PHOSPHOPACH, SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%; Score 19; DB 2; Length 3935;
57.1%; Pred. No. 2.6e+04;
iive 0; Mismatches 3; Indels
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Last annotation update)
                                Bacteria; Cyanobacteria; Oscillatoriales; Lyngbya.
NCBI_TaxID=158786;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein,
OrderedLocusNames=LA3643;
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les 4; Conservative
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                   majuscula
                                                                                          SEQUENCE FROM N.A.
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Q8F054;
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Q8F054
LD Q8F055
AC Q8F055
DT 01-MAN
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808088
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SEQUENCE FROM N.A.

STRAIN=SeGOL / Serogroup Icterohaemorrhagiae / Serovar lai;
STRAIN=SeGOL / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204; DOI=10.1038/mature01597;
A. Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miaco Y.-G., Xu H.,
A. Zhang Y.-X., Gu W.-Y., Zhang Y.-O., Jiang H.-P., Jiang H.-P., Jiang Y.-X., Gu W.-Y., Zhang Y.-C., Gai Z., Sheng H.-H., Yin H.-F.,
A. Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Xu O.Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guc X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
A. Xu J.-G., Zhao G.-P.;
"Unique physiological and pathogenic features of Leptospira
Interrogans revealed by whole-genome sequencing.";
In Nature 422:888-893(2003).
R. EMBL; AEO11520; AAN50841.1; -.
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PubMed=15057449;
Yang Y.C., Chou C.P., Kuo T.T., Lin S.H., Yang M.K.;
Yang Y.C., Chou E.P., Kuo T.T., Lin S.H., Yang M.K.;
PpilR enhances the sensitivity of Xanthomonas axonopodis pv. citri to the infection of filamentous bacteriophage Cf.";
Curr. Microbiol. 48:251-261(2004).
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Pred. No. 8.3e+02;
0; Mismatches 3; Indels
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SEQUENCE 39 AA; 4743 MW; AF11ED6D2C89107B CRC64;
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01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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(Rel. 27, Last sequence update)
(Rel. 44, Last annotation update)
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Similarity 57.1%;
4; Conservative
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Gaps

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Indels

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Pubmed=1244438; DOI=10.1038/nature01184;
Pubmed=1244438; DOI=10.1038/nature01184;
Pubmed=1244438; DOI=10.1038/nature01184;
A Sasaki T., Matsumcto T., Yamamoto K., Sakata K., Baba T., Katayose Y., An U. J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., A. Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Itch T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Karagawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., An Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Najasaki M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Nakai K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Golobori T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Wallen M., Jang J., Golobori T., Ito Chromosome I.";
                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P045-9B04.5 protein (P0658H10.23 protein).
Name=P0459B04.5; Synonyms=P0698H10.23;
Oryza sativa (japonica cultivar-group).
Usukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ephrattoideae; Oryzeae; Oryza.
NUBL TAXID=39947;
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activity; IEA.
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Last annotation update)
Pred. No. 1.4e+03;
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Pred. No. 1.5e+03;
1; Mismatches 3;
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GO, GO:0005743; C:mitochondrial inner membrane, GO, GO:0005655; F:protein transporter activity, GO, GO:0015031; P:protein transport; IEA. InterPro; IPR003397; Tim17_Tim22.
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                                                                 0; Mismatches
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Local Similarity 42.9%;
les 3; Conservative
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                              57.1%;
                                                                 4; Conservative
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                                                                                                                                                                                                42 VGTSAEF 48
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                                  Best Local Similarity
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Q854J0;
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Matches
                                                                 Matches
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Biochemistry 33:5098-5108(1994).

-!- FUNCTION: Omega-agatoxins are antagonists of voltage-sensitive calcium channels. This toxin is a potent blocker of N-type calcium channels. It also blocks L-type calcium channels, but with less potency than omega-Aga-IIIA. It does not block T-type channels. It blocks calcium currents in locust thoracic neurones, but does not block housefly neuromuscular transmission presynaptically.
                                                                                                                                                                                                                                                                                                                                                                                                              Parol. Biol. 267:2610-2615(1992).

-1- FUNCTION: Omega-agatoxin are antagonist of voltage-sensitive calcium channels. They block insect neuromuscular transmission presynaptically. Potent blocker of N- and L-type calcium channels.
-1- SUBCELLUIAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed by the venom gland.
-1- FTM: Contains six disulfide bonds (Probable).
-1- SIMILARITY: Belongs to the omega-agatoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Caclcium Cahanel inhibitor; Direct protein sequencing;
Ionic channel inhibitor: Neurotoxin; Presynaptic neurotoxin; Toxin.
SEQUENCE 76 AA; 8518 MW; 6A715CAC9591888B CRC64;
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                                                                                                                                                                                                                                                          TISSUE-Venom;
PEDLINE-2921293151; PubMed=1310319;
Venema V.J., Swiderek K.M., Lee T.D., Hathaway G.M., Adams M.E.;
"Antagonism of synaptosomal calcium channels by subtypes of omega-
                                                   Agelenopsis aperta (Funnel-web spider).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Araneomorphae, Entelegynae, Agelenidae, Agelenopsis.
NCBI_TaxID=6908;
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Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, VARIANTS SER-29 AND ARG-35, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 1; Length 76; 57.1%; Pred. No. 1.46+03; ive 0; Mismatches 3; Indels
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-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- PTM: Contains six disulfide bonds (Probable).
-!- SIMILARITY: Belongs to the omega-agatoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium channel inhibitor; Direct protein sequencing;
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
06-JUL-2004 (Rel. 44, Last annotation update)
Agelenopsis aperta (Funnel-web spider).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 AA.
                           Omega-agatoxin IIIA (Omega-Aga-IIIA)
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MEDLINE=94227039; PubMed=8172884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6908;
                                                                                                                                                                                                                                                                                                                                                                                             agatoxins.";
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith M.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
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30 VGSSAEF 36
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Best Local Similarity
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41
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92 AA;
  NCBI_TaxID=10141;
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MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2; Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Ralbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                     Name=B1120F06.135; Synonyms=B1272H04.1;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P20658;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Protein 10 (29 KDa calcium-binding protein, brain-specific)
(Fragments)
                                                                                                                               Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
clone:B1272H04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 2; Length 88; 57.1%; Pred. No. 1.6e+03;
                                                                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                               05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1120F06.135 (Hypothetical protein
B1272H04.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AP005830; BAC84533.1; -. EMBL; AP006479; BAD32057.1; -.
                                                                    "Origins of highly mosaic mycobacteriophage genomes."; Cell 113:171-182(2003).
[Embl. AY129338; AAN12718.1; - SEQUENCE 88 AA, 10324 MW; SD13C1010CA698SE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 88 AA; 10001 MW; 693B4D3224B4D010 CRC64;
                                                                                                                             81.8%; Score 18; DB 2; I
57.1%; Pred. No. 1.6e+03;
tive 0; Mismatches 3;
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4; Conservative
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les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone: B1120F06."
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Q6YVE3;
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CAVPO
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsurnoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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DAR Res 9:189-197 (2002).
EMBL; AP005936; BAC45816.1; -.
GO; GO:0016020; C:membrane; IEA.
TISSUB=Brain;
MEDLINE=9009311; PubMed=2602362;
MEDLINE=9009311; PubMed=2602362;
Winsky L., Nakata H., Martin B.M., Jacobowitz D.M.;
"Isolation, partial amino acid sequence, and immunohistochemical localization of a brain-specific calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:10139-10143(1989).
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                     -!- MISCELLANEOUS: Binds calcium.
-!- SIMILARITY: Belongs to the calbindin family.
-!- SIMILARITY: Contains 6 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

81.8%; Score 18; DB 2; Length 96;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 1; Length 92;
Pred. No. 1.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11067 MW; D1CCD66C148A7F6A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                PIR, A34520; A34520.
InterPro; IPR002048; EF-hand.
InterPro; IPR010989; EF Hand like.
PROSITE; PS00018; EF HAND; PARTIAL.
Calcium-binding; Direct protein sequencing.
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Pfam; PF02325; YGGT; 1.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bs10551 protein.
OrderedLocusNames=bs10551;
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13 VQSTAEF 19

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RESULT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

PubMed=1522959; DOI=10.1038/nature02579;

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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Bayne E., Bleykasten C.,

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Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

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T "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 430:35-44(2004).

-! FUNCTION: Important for transcription initiation. The SPT4/5/6

-! FUNCTION: Important for transcription initiation. It may normally complex is required for transcription initiation. It may normally act to repress transcription at a variety of loci, and also plays a role in chromatin structure or assembly. Metal binding is important for its function (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                          Hikkel I., Gbelska Y., Subik J.;
"Identification and functional analysis of a Kluyveromyces lactis homologue of the SPT4 gene of Saccharomyces cerevisiae.";
Curr. Genet. 34:375-378(1998).
                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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869070285CF7917C CRC64;
                                                                                                                                    15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-DCT-2014 (Rel. 45, Last annotation update)
Name=SPT4; OrderedLocusNames=KLLAOB07997g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF06093; Spt4; 1.
Nuclear protein; Transcription; Zinc-finger.
                                                                                   102 AA.
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                                                                                                                                                                                                                                                                                                                            MEDLINE=99087905; PubMed=9871119;
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                                                                                                                  15-JUL-1998 (Rel. 36, Created)
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                                                                                   STANDARD;
41 VSAVAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                              MEDLINE=22555705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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                                                                                                                                                        Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveelata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 57.1%; Pred. No. 1.9e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raser C.M., Barrell B.;
Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A2177839; CAB90828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AA; 11716 MW; 0129998AEB88770C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA.
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                                                                                         Last sequence update)
Last annotation update)
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                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last anno
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006662; Thiored.
InterPro; IPR005746; Thioredoxin.
InterPro; IPR006663; Thioredox_dom2.
                       PRT;
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                       PRELIMINARY;
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Matches
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27KQL8
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"Arthrobacter aurescens TC1 Atrazine Catabolism Genes trzN, atzB, and atzC Are Linked on a 160-Kilobase Region and Are Functional in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGUENCE FROM N.A.
SETRAIR-S288C (A M8972)
MEDLINE-9731326; PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.",
Nature 387:84-1871997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher B. Y., Vannberg F., Weger J., Kramer J., Moreixa D., Kelley F., Zoo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A., Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LaBaer J.;
"Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical 13.0 kDa protein in SNPI-GPP1 intergenic region.
                                                                                                                                                                                                                                                            Similarity 57.1%; Pred. No. 2e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                   7 23 Potential.
121 AA; 13030 MW; 18B23D652939CDD2 CRC64;
                                atzc Are minoca ...
Becherichia coli.";
Appl. Environ. Microbiol. 70:4402-4407(2004)
EMBL; AY456696, AA520147.1; -.
InterPro; IPR0108651; HicB.
InterPro; IPR010985; Met_repress_like.
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GermOnline; 139596; -.
SGD; S000001321; YIL059C.
Hypothetical protein; Transmembrane.
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EMBL; AY693258; AAT93277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=YIL059C;
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                                                                                                                                                                                                                                                                                                                                                                                                         26 VATVÁÉF 32
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P40520;
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                                                                                                                                                                                                                                                                                                                Gaps
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PubMed=15240330; DOI=10.1128/AEM.70.7.4402-4407.2004;
Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B.,
Tomkins J., Sadowsky M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                            81.8%; Score 18; DB 2; Length 104; 57.1%; Pred. No. 1.9e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from an endophytic Streptomyces sp.";
Plaemid 49:86-92(2003).
EMBL, AFS33985, AAN76283.1; -.
Hypothetical protein; Plaemid.
SEQUENCE 106 AA; 11488 MW; E2B127026C785A91 CRC64;
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Last annotation update)
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Last annotation update)
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GO:0006118; P:electron transport; IEA.
                   InterPro; IPR006662; Thiored.
InterPro; IPR005746; Thioredoxin.
InterPro; IPR00663; Thioredox dom2.
Pfam; PF00085; Thioredoxin; 1.
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                        TIGRFAMB; TIGR01068; thioredoxin; 1. PROSITE; PS00194; THIOREDOXIN; 1.
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                                                                                                                                                                                                                                                                                                             4; Conservative
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les 4; Conservative
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Plasmid pEN2701.
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065K25
AC 065K2
AC 065K2
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DT 0
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moser, 60:0003677; F:DNA binding; IEA.
GO; GO:0000156; F:two-component response regulator activity; IEA.
GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF220046; AAF67639.1; -. GO; GO:0000159; C:protein phosphatase type 2A complex; IEA. GO; GO:0000159; C:protein phosphatase type 2A regulator activity; IEA. GO; GO:0007165; P:signal transduction; IEA. InterPro; IPR011044; Amine DH B_like. InterPro; IPR000009; Pp2A_PR55.
 predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Uncharacterized hematopoietic stem/progenitor cells protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                 Score 18; DB 2; Length 134;
Pred. No. 2.4e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 2; Length 137; 57.1%; Pred. No. 2.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                  PROSITE; PS50110; RESPONSE RECULATORY; 1.
Complete proteome; Phosphorylation; Sensory transduction.
SEQUENCE 134 AA; 15035 MW; A76AF72470EA58EF CRC64;
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Last annotation update)
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                                                                                                                                 InterPro; IPR011006; Chev_like.
InterPro; IPR001109; Response_reg.
Pfam; PP00072; Response_reg;
ProDom; PD000039; Response_reg; 1.
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57.1%;
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                 genomic perspective.";
Science 303:689-692(2004).
EMBL; BX842652; CAE80226.1;
HSSP; P06143; 1AB6.
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                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                       SM00448; REC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VITAÄEF 13
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
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Q9NZ48
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CATAIN=CZA / ATCC 35395 / DSM 2834;

STRAIN=CZA / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;

A Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

A Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Linton L., Maran-Smith C., Kuettner H.C., Krzycki J.A.,

A Hedderich R., Ingara-Smith C., Kuettner H.C., Krzycki J.A.,

A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Perry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,

Metcalf W.W., Birren B.;

A Metcalf W.W., Eirren B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."; Genome Res. 12:532-542(2002).
                                    Gaps
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PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.E., Schuster S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
NCBI_TaxID=959;
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                                                                                                                                                                                                                                                                                                    Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
Score 18; DB 1; Length 121; Pred. No. 2.2e+03;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 2; I
57.1%; Pred. No. 2.2e+03;
                                                                                                                                                                                      123 AA
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                                 0; Mismatches
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              57.1%;
 81.8%;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                     OrderedLocusNames=MA3803;
                                 4; Conservative
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                                                                                                VTALAEF 25
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                                                                1 VXXXAEF 7
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               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 123 AA
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2214;
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 Query Match
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Q8TJ11
                               Matches
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InterPro; IPR002177; DPS.
InterPro; IPR009078; Perritin/RR_like.
InterPro; IPR008331; Perritin_Dps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 81.8%;
Similarity 57.1%;
4; Conservative (
  OrderedLocusNames=VNG1907H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00210; Ferritin; 1.
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HSSP; P80725; 1QGH.
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
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SEQUENCE 147 AA
                                                                                                  NCBI_TaxID=64091;
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A MEDLINE=9740, 25; PubMed=9256512; DOI=10.1073/pnas.94.17.9504;
A Pohlmeyer K., Soll J., Steinkamp T., Hinnah S., Wagner R.;
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T protein present in the chloroplastic outer envelope membrane.";
D Proc. Natl. Acad. Sci. U.S.A. 94:9504-9509(1997).
R EMBL; Z73553; CAA97910.1; -.
R PIN; T06471; T06471.
R GO; GO:0005743; C:mitcochondrial inner membrane; IEA.
GO; GO:0005743; C:mitcochondrial inner activity; IEA.
R GO; GO:0015743; C:mitcochondrial inner membrane; IEA.
R GO; GO:0015743; Timitcochondrial inner membrane; IEA.
R GO; GO:0015741; Timitcochondrial inner membrane; IEA.
R GO; GO:00157456; Timitrochondrial inner membrane; IEA.
R DitterProc. IPR003397; Timitcochondrial inner membrane; IEA.
R Pam; PF02466; Timitrochondrial inner membrane; IEA.
R Pam; PF02466; Timitrochondrial inner membrane; IEA.
R Pam; PF02466; Timitrochondrial inner membrane; IEA.
                                                                                DEQUENCE FACTOR N.A.

STRAIN-CGA009 / ATCC BAA-98;

PubMed=14704707; DOI=10.1038/nbt923;

PubMed=14704707; DOI=10.1038/nbt923;

PubMed=14704707; DOI=10.1038/nbt923;

PubMed=14704707; DOI=10.1038/nbt923;

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"Complete genome sequence of the metabolically versatile

photosynthetic bacterium Rhodopseudomonas palustris.";

Patty December 122.7687.1;

EMBL; BX572600; CAE27687.1;

Complete proteome; Hypothetical protein.

SEQUENCE 141 AA; 15197 MW; BE25F6A6E9C28C51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum. NCBI_TaxID=3888;
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42.9%; Pred. No. 2.6e+03;
iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 2; Length 141; 57.1%; Pred. No. 2.5e+03; ive 0; Mismatches 3; Indels
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Last annotation update)
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Last annotation update)
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Bradyrhizobiaceae; Rhodopseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24,
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Matches 4; Conservative
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                                                                         SEQUENCE FROM N.A.
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                         NCBI_TaxID=1076;
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1041050

AC 041050

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MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

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Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

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MEDLINB=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Non-heme iron-binding ferritin.
Name-dpsA; OrderedLocusNames=LL2025;
Lactococus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea, Buryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length 147; Pred. No. 2.6e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 57.1%; Pred. No. 2.6e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA; 15759 MW; F83795F6D0D64204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AA; 16653 MW; 8424544D9AFEB097 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0008199; F:ferric iron binding; IEA. GO; GO:0006879; P:iron ion homeostasis; IEA. GO; GO:0006950; P:response to stress; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactis ssp. lactis IL1403.";
Genome Res 11.731-753 (2001).
-!- SIMILARITY: Belongs to the dps family.
EMBL; AE006432; AAKO6123.1;
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PIR; C87486; C87486
                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 151 AA;
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          NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUCR
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9A714;
                                                                                                                                                                                                                                                                                                                                                                                                                       FABZ_CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                      FABZ
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                       STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674; DOI=10.1073/pnas.0401356101;
Fuetteerer O., Angelov A., Liesegang H., Gottechalk G., Schleper C., Schepers B., Dock C., Antranikian G., Liebl W.;
"Genome sequence of Picrophilus torridus and its implications for life around pH 0.";
                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 101:9081-9086 (2004).

-1- FUNCTION: This protein binds specifically to 23S rRNA. It makes multiple contacts with different domains of the 23S rRNA in the assembled 50S subunit and ribosome (By similarity).

-1- FUNCTION: The globular domain of the protein is located near the polypeptide exit tunnel on the outside of the subunit, while an extended beta-hairpin is found that lines the wall of the exit tunnel in the center of the 70S ribosome (By similarity).

-1- SUBUNIT: Part of the 50S ribosomal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_0133; -; 1.
ProDom; PD01032; Ribosomal_L22; 1.
PROSITE; PSO0464; RIBOSOMAL_L22; FALSE NEG.
COMPLETE PROCEME; RIBOSOMAL_D20: FALSE NEG.
COMPLETE PROCEME; RIBOSOMAL protein; RNA-binding; RNA-binding.
SEQUENCE 149 AA; 16731 MW; A80FA918151BA217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                      Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
NCBI_TaxID=82076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 1; Length 149; 57.1%; Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                      25-OCT-2004 (Rel. 45, Last Sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 50S ribosomal protein L22P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA.
                                                                                                    149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                               Name=rpl22p, OrderedLocusNames=PT00645;
Picrophilus torridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                           25-OCT-2004 (Rel. 45, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE017261; AAT43230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blr6079 protein.
OrderedLocusNames=blr6079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                  69 VSTLAEF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 VSANAEF 98
         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VXXXAEF 7
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
         VXXXAEF
                                                                                                  PICTO
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                                                                                                            Q6L1C2;
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                                                                                      RL22_PICTO
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0894B8
1D 0894B
AC 0894B
DT 01-JU
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DT 01-JU
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28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
(3R)-hydroxymyristoyl-{acyl carrier protein} dehydratase (EC 4.2.1.-)
(3R)-hydroxymyristoyl ACP dehydrase).
Name=fabZ, OrderedLocusNames=CC1912;
                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Matanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN=ATCC 19089 / CB15;
MEDLINE=21173699; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE=21173699; PubMed=11259647; DOI=10.1073/pnas.061029298;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Maddock J.R.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DANA Res. 9:189-197(2002).
EMBL; AP005957; BAC51344.1; -
GO: GO:0045735; F:nutrient reservoir activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: Involved in saturated fatty acids biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (9 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 2; Length 151;
57.1%; Pred. No. 2.6e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA; 16840 MW; 7AAAD1AC94717AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin region.
InterPro; IPR011051; RmlC_like_cupin.
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                                                                                                                                                                                           MEDLINE=22484998; PubMed=12597275;
Bradyrhizobiaceae; Bradyrhizobium.
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Kenopus laevis (African clawed frog)
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                                                                 Xenopodinae; Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ^
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                      TISSUE=Intestine;
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                                                                                       NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                          Gaps
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Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
TIGR; CC1912; -.
HAWAP: MF 00406; -; 1.
InterPro; IPR010084; Fabz.
InterPro; IPR0106683; Thiosetr_supf.
EngrEAMs; PF03061; 4HBT; 1.
TIGREAMs; TIGR01750; fabz; 1.
TIGREAMs; TIGR01750; fabz; 1.
AT SITE 59 By simllarity.
SEQÜENCE 159 AA; 17443 MW; 2C7EAA86668EA0141 CRC64;
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MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 18; DB 2; Length 171;
57.1%; Pred. No. 3e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                              81.8%; Score 18; DB 1; Length 159. 57.1%; Pred. No. 2.8e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Protein phosphatase 2 regulatory subunit B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE=22608306; PubMed=12692562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
                                                                                                                                                                                                                                  Local Similarity 57.1 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=SAV60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                           142 VAAEAEF 148
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                                                                                                                                                                                                                                                                                                 1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-JUN-2003
                                                                                                                                                                                                              Query Match
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Q9DDR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q82RT3
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10 202RT3
10 202RT3
10 10-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
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Q9DDR2
ID Q9DDR
AC Q9DDR
DT 01-MAD
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DE Prote
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

STAIR=CZA / ATCC 35395 / DSM 2834;

STAIR=CZA / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932238; DOC=10.1101/gr.223902;

A dalagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., A rizthush W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., A inton L., McKernan R., Talamas J., Tirrell A., Ye W., Linton L., McKernan F., Koetrner H.C., Krzycki J.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Guss A.M., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Mctchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., A mtchelmosarcina acetivorans reveals extensive metabolic Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson M.D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 3 WD repeats.

-!- SIMILARITY: Contains 3 WD repeats.

GO; GO:0000159; C:protein phosphatase type 2A complex; IEA.

GO; GO:0000651; F:protein phosphatase type 2A regulator activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR010049; PD2A_PRSE.

InterPro; IPR010009; PD2A_PRSE.

InterPro; IPR010009; WD40.
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                                                                                                                                                                                                                                                      Minter R., Horton J.D., Watson M.D.;
"Development of Antibody Technology to Identify Natural Killer Cell
"Surface Antigens in Xenopus laevis.";
Thesis (1999), University of Durham, South Rd., Durham, UK.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Name=pfpl; OrderediocusNames=WA1654;
Name=pfpl; OrderediocusNames=WA1654;
Archanosarcina acetivorans.
Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 2; Length 173;
Pred. No. 3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 AA; 20210 MW; BD84B23CA0F80880 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
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SMART; SMO0320; WD40; 3.
PROSITE; PSO1025; PR55_2; 1.
Repeat; WD repeat.
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Best Local Similarity 5/...
Best A; Conservative
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WormBase; WBGene00022115; Y71F9AL.10
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[1]
SEQUENCE FROM N.A.
                                                                                                                    FROM N.A.
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                                                                                                                    SEQUENCE
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Q9N416;
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Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
de Oliveira J.C.P., Wood D., de Oliveira M.C., Miyaki C.Y.,
Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,
Ferro M.I.T., Gagliardi P.R., Giglioti E., Goldman M.H.S.,
Goldman G.H., Kimura E.T., Perro B.S., Kuramae E.E., Lemos E.G.M.,
Lemos M.V.P., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.,
"The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
xyli subsp. xyli.",
Mol. Plant Microbe Interact. 17:827-836(2004).
                                                                                                                                                                                                Gaps
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Viruses, dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=227470;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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42.9%; Pred. No. 3.2e+03;
tive 1; Mismatches 3; Indels
                                                                                                                                                       Length 179;
                                                                                                                                                                                              3; Indels
                                 GO; GO:0008233; F:peptidase activity; IEA.
InterPro; IRR002818; ThiJ/PfpI.
Pfam; PF01965; DJ-1PfpI; 1.
Complete proteome; Protease; SEQUENCE 179 AA; 19359 MW; E0FDC30D4BF4P456 CRC64;
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Last annotation update)
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Pred. No. 3.1e+03;
0; Mismatches 3;
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NCBI_TaxID=59736;
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EMBL; AE010838; AAM05062.1; -
                                                                                                                                                       81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                Query Match
Best Local Similarity 57.11,
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ORFNames=AehlORF102c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                           38 VTVAAEF 44
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IAATAEF 95
                    059413; 1G2I.
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nes 3; Conserv
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SEQUENCE 184 AA
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PubMed=15305603;
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Q6AC19;
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06AC19
1D QGAC19
DT 25-0C
DT 25-0C
DT 25-0C
DF HYPOT
GGN Leife
GGN
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Matches
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M.,
Karam J.D.;
                                                                                                                                                                                                                                                                                Length 186;
                                                                                                                                                                                                                                                                          Score 18; DB 2; Length 186
Pred. No. 3.2e+03;
0; Mismatches 3; Indels
                                                                                                                    Petrov V., Nolan J., Karam J.D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY266303; AAQ1763.1; ...
Hypothetical protein.
SEQUENCE 186 AA; 21839 MW; 45060CC5F8B03B11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
Bradshaw-Cordum H., Scott K., Graves T.,;
"The sequence of C. elegans cosmid Y11F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last anno
Hypothetical protein Y71F9AL.10.
Name=Y71F9AL.10; ORFNames=Y71F9AL.10;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
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57.1%;
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Best Local Similarity 57...
Best Local 4; Conservative
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193 AA.

PRT;

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PRELIMINARY;
                     01-MAR-2003
01-MAR-2003
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Q63EZ7;
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A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Abjele M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Oziar-Kalogeropoulos O.,
Pellenz S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Weethof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T., "Genome evolution in yeasts.";
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                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                    ORFNames=YAL10B21274g;
Yarrowia lipolytica CLIB99.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                             Length 189;
       GO; GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004642; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; F:protein ubiquitination; IEA.
FINTERPRO. | IRRO10841; Znf ring.
FEAN; PFO0097; Zf-C3HC4; I.
                                                                                                                                           81.8%; Score 18; DB 2; Length 189
57.1%; Pred. No. 3.2e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                               SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 189 AA; 21048 MW; 7BDA2D05F0362CD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CR382128; CAG83427.1; -.
SEQUENCE 193 AA; 22016 MW; 939292835977B6BF CRC64;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                         Created)
WormPep; Y71F9AL.10; CE31386.
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                                                                                                                               Ouery Match
Best Local Similarity 5/...
4; Conservative
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                                                                                                                                                                                                                   37 VMTAAEF 43
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RESULT 80 Q8E1V1

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                                                                                                                                                                                                                                                                                                                                        STRAIN=2603 V/R / Serotype V;
MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Tettellin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Wulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchardon P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.;
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
"Complete Genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU19332.1; -.
SEQUENCE 194 AA; 22360 MW; CCCECE4FIC508863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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                                                                                                                                                   Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus ZK.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AA; 22090 MW; 06D80D9E108F8159 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Group-specific protein.
                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Created)
                                                                                     Membrane protein, putative.
OrderedLocusNames=SAG0250;
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Matches 4: Conserv
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE 193 AA
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Ikeda H., Ishikawa J.; Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Mat. Biotechnol. 21:526-531(2003).
EMBL, AP005030; BAC70111.1;
GO, GO:0003824; F:catalytic activity; IEA.
                                                                                                                                                                                                                                                  InterPro; IPR006683; Thioestr_supf...
Pfam, PR03061; 4HBT; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 194 AA; 20316 MW; 3BE41F14E45228D5 CRC64;
   MEDLINE=22608306; PubMed=12692562;
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57.1%;
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Best Local Similarity 57.1..,
A; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kleser H.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces
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MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 2; Length 194; 57.1%; Pred. No. 3.3e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Hypothetical protein.
SEQUENCE 194 AA; 20474 MW; 9FE391B9E3CED80E CRC64;
                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
1-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein SCO5867.
ORFNames=SC2E9.08;
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Last annotation update)
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                                                                 194 AA.
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Nature 417:141-147(2002).
BEMBL, A1939125; CAA16476.1; -.
PIR; T34819; T34819.
GO; GO: 003824; F: catalytic activity; IEA.
PIRTEPPO; IPR006683; Thioestr_supf.
Pfam; P903061; 4HBT; 1.
                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
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                                                              PRELIMINARY;
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0082KK3
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RESULT 82
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REQUENCE FROM N.A.

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REA MIDELINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;

RA VOSCONCEOLOS A.T.R., de Almeida D.F., Hungria M., Guimaraees C.T.,

RA Antonio R.V., Almeida F.C., de Almeida E.G.P., de Araujo M.F.F.,

Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Batista J.S., Belo A., Van den Berg C., Bogo M., Bonatto S.,

RA Garranco C.M., Cascardo J.C.M., Cavada B.S., Chueiro B.N.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Ferrari L.P., Ferro G.T.,

RA Ferro M.I.T., Franco G.R., Frelipe M.S., Ferrari L.P., Ferro J.A.,

RA Gazzinelli R.T., Gomes B.A., Goncalves P.R., Grangeiro T.B.,

RA Gazzinelli R.T., Gomes B.A., Loureiro M.F., Lyra M.C.C.P.,

RA Gazzinelli R.T., Gomes B.A., Loureiro M.F., Lyra M.C.C.P.,

RA Madeira H.M.F., Manfio G.F., Maranhao A.Q., Martins W.S.,

A di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.,

RA Paixao R.F.C., Parente J.A., Pederosa F.O., Pena S.D.J., Pereira J.O.,

RA Paixao R.F.C., Parente J.A., Pederosa F.O., Pena S.D.J., Rerianto-Neto C.E., Reis A.M.M., Rigo L.U., Soulza B.N.,

Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,

Santos B.B.P., Santes R.B., Soares R.B., Souza B.M., Stepholocker, 
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Score 18; DB 2; Length 194; Pred. No. 3.3e+03; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MMR-2004 (TrEMBLrel. 26, Created)
01-MMR-2004 (TrEMBLrel. 26, Last sequence update)
01-MMR-2004 (TrEMBLrel. 26, Last annotation update)
Molybdopterin-quanine dinucleotide biosynthesis protein.
Name=mobA, OrderedLocusNames=CV1625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AA.
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81 VTNAAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. SR1; TISSUE=Leaf;
MEDLINE=93027271; PubMed=1408841;
Hansen G., Estruch J.J., Spens A.;
"Tobacco cDNA encoding the ribosomal protein S6.";
Nucleic Acids Res. 20.5230-52310(1992).
- !- FUNCTION: May play an important role in controlling cell growth and proliferation through the selective translation of particular
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Ribosomal protein S6 is the major substrate of protein kinases in eukaryote ribosomes.
-!- SIMILARITY: Belongs to the ribosomal protein S6e family.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 1; Length 199; 57.1%; Pred. No. 3.4e+03;
Pred. No. 3.4e+03;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Stretchin-MLCK (Fragment).
                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
40S ribosomal protein S6 (Fragment).
                                                                                                                                                                                                                                                  199 AA
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                                              0; Mismatches
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InterPro; IRR001377; Ribosomal S6E.
Pfam; PF01092; Ribosomal S6e; I.
ProDor PD000460; Ribosomal S6e; I.
PROSITE; PS00578; RIBOSOMAL S6E; I.
Phosphorylation; Ribosomal Fxotein.
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                    57.1%;
                                              4; Conservative
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ses 4; Conservative
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                         Best Local Similarity
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                                                                                         1 VXXXAEF 7
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                                                                                                                                                                                                                                               RS6_TOBAC
P29345;
                                                                                                                                                                                                                                                                                                                                                                                   Name=RPS6;
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TO THE TO THE
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GO; GO:0004685; F:calcium- and calmodulin-dependent protein k. . .; IDA.
GO; GO:0004687; F:myosin-light-chain kinase activity; IDA.
InterPro; IPR001599; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CIP102578; PubMed=7828933; DOI=10.1016/0378-1119(94)00692-L; MEDLINE=9112920; PubMed=7828933; DOI=10.1016/0378-1119(94)00692-L; Elisha B.G., Courvalin P.; "Analysis of genes encoding D-alanine:D-alanine ligase-related enzymes in Leuconostoc mesenteroides and Lactobacillus spp.";
                                                                                                                SEQUENCE FROM N.A.
MEDINE20351481; PubMed=10891286; DOI=10.1006/jmbi.2000.3802;
Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
"Drosophila stretchin-MLCK is a novel member of the Titin/Myosin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 57.1%; Pred. No. 3.4e+03; 4; Conservative 0; Mismatches 3; Indels
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201 AA; 22150 MW; CFC118FDC3C423DD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Lactobacillales; Weissella.
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InterPro; IPRO11127; Dala_Dala_lig_N.
Pfam; PF07478; Dala_Dala_lig_C; 1.
Pfam; PF01820; Dala_Dala_lig_N; 1.
                                                                                                                                                                                                                   chain kinase family.";
7. Mol. Biol. 300:759-777 (2000).
EMBL; AF257311; AAF90129-1;
HSSP; Q9UQH9; 1DJS.
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
SMART; SM0409; IG; 2.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 152:79-83(1995).
EMBL; U08910; AAA87680.1; -.
HSSP; P71454; 1EHI.
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   baculovirus infection.";
Virology 268:56-67(2000)
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  O6VTX4
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Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
"Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
EMBL; AP006841; BAD47782.1; -.
Hypothetical protein.
SEQUENCE 211 AA; 24442 MW; C86EC7A0D93BA917 CRC64;
                                                                                                                                                                                                                                                                                                                 PubMed=15240330; DOI=10.1128/AEM.70.7.4402-4407.2004; Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B., Tomkins J., Sadowsky M.J.; "Arthrobacter aurescens TCl Atrazine Catabolism Genes trzN, atzB, and atzC Are Linked on a 160-Kilobase Region and Are Functional in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococineae, Micrococcaceae, Arthrobacter.
NCBL_TaxID=43663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 18; DB 2; Length 211; 57.1%; Pred. No. 3.6e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 2; Length 207; 57.1%; Pred. No. 3.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Plasmīd.
SEQUENCE 207 AA; 21741 MW; F10397D13AD2F10A CRC64;
                                        Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL, AX456696; AAS20024.1; -...
InterPro; IPR001763; Rhodanese-like.
Ffam; PF00581; Rhodanese; 1.
SMART; SM00450; RHOD, 1.
PROSITE; PS50206; RHODANESE 3; 1.
207 AA
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PRT;
                                          (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteroidaceae; Bacteroides NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.1 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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PRELIMINARY;
                                                                                                           Hypothetical protein.
Arthrobacter aurescens.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
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                                                                                                                                                           Plasmid pAA1
                                        05-JUL-2004
05-JUL-2004
                                                                                        05-JUL-2004
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Q6SKE7
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Q64XJ4
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RESULT 90

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A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aaje M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Rerry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lewsur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Oztar-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.,
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Yarrowia lipolytica CLIB99.
Eukaryota; Fungi Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                     MEDICALE 20149221; PubMed=10683327; DOI=10.1006/viro.1999.0138; Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.; "Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 81.8%; Score 18; DB 2; Length 211; Best Local Similarity 57.1%; Pred. No. 3.6e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                           Choristoneura fumiferana defective nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY327402; AAQ91712.1;
-.
InterPro; IPR009661; DUF1251.
Fram: PF06666; DUF1251.
Hypothetical protein.
SEQUENCE 211 AA; 23673 MW; A24E6286DF93CA3A CRC64;
                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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Last annotation update)
  211 AA.
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PRT;
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MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
Parkhill J. Wren B W., Mungall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Witheread S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:65-668 (2000).
EMBL, AL139076; CAB73007.1; -.
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MEDLINE-21359325; PubMed=11466286;
DOI=10.1128/JUB.183.16.4823-42001;
DOI=10.1128/JUB.183.16.4823-42001;
Doelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Tatusov R.L., Bennett G.N., Koonin E.V., Smith D.R., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridum acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0016791; F:phosphoric monoester hydrolase activity; IEA.
GO; GO:0016791; P:phosphoric monoester hydrolase activity; IEA.
InterPro; PR005834; Debal like hydro.
InterPro; IPR005831; HAD SF IB.
InterPro; IPR005885; HAD SF IB.
PFam; PF00702; Hydrolase; 1.
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GO; GO:0016791; F:phosphoric monoester hydrolase activity; IEA.
GO; GO:000152; P:metabolism; IEA.
InterPro; IPR006383; HAD SF IE.
InterPro; IPR006385; HAD SF IE hyp2.
TIGRFAMS; TIGR01488; HAD-SF-IE, 1.
TIGRFAMS; TIGR01490; HAD-SF-IE-hyp1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18, DB 2; Length 212;
Pred. No. 3.6e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO1488; HAD-SF-IB; 1.
TIGRFAMS; TIGRO1490; HAD-SF-IB-hypl; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 212 AA; 25015 WW; RAR92FEBBDF54ED4 CRC64;
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01-077-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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OrderedLocusNames=CAC2227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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J. MOI. Biol. 3000:759-777 (2000).

EMBL; AF257310; AAF90128.1; ---

HNSP; Q9UQH9; 1DJS.

FlyBase; FBGN013988; Strn-Mick.

GO; GO:0004687; F:calcium- and calmodulin-dependent protein k. .; IDA.

GO; GO:0004687; F:myosin-light-chain kinase activity; IDA.

InterPro; IRR00710; IG-like.

SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                            Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 2; Length 212; 57.1%; Pred. No. 3.6e+03; cive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                        3; Indels
                                          to the EMBL/GenBank/DDBJ databases.
             Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR382122; CAG83321.1; -.
SEQUENCE 212 AA; 24023 MW; 95219C003E2B41E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA; 23599 MW; 5DC06D88FD2B4803 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                   Score 18; DB 2; I
Pred. No. 3.6e+03;
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                                                                                                                                                                          81.8%;
57.1%;
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01-0CT-2000 (TrEMBLrel. 15, I
01-MAR-2004 (TrEMBLrel. 26, I
Hypothetical protein Cj0733.
OrderedLocusNames=Cj0733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QANDDO,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stretchin-MLCK (Fragment).
                                                                                                                                         4; Conservative
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SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
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090NB0
1D 090NBB
AC 090NBB
AC 01-0C
DT 01-0C
DT 01-M
DE Strei
GN Name
OC Euka
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O9PPH4
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AC 09PPH
AC 01-0C
DT 01-NAC
DT 01-MAC
DE HYPOT
CAMPY
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DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Pleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL, AAABO1008960; EAA11056.1; -.
SEQUENCE 217 AA; 24420 MW; FSAICC770B728ECB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 57.1%; Pred. No. 3.7e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                 22587 MW; 423CD8B32A67B7A8 CRC64;
                                                                                                                                                                                                                                                                Ol-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP6282 (ENSANGP00000018110).
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                             Score 18; DB 2; I
Pred. No. 3.7e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                      Name=agCG52667; Synonyms=ENSANGG0000015621;
ORFNames=ENSANGG0000015279;
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NCBI_TaxID=837;
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MEDLINE=22829867; PubMed=12949112;
                                                 81.8%;
57.1%;
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OrderedLocusNames=PG1823;
                                                                                  4; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
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                 216 AA;
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                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                  1 VXXXAEF 7
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Complete proteome. SEQUENCE 216 AA;
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Q7MTV9
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                                                                                                                                                                                                                                                                                                             MEDLINE=20351481; PubMed=10891286; DOI=10.1006/jmbi.2000.3802; Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.; Edwards K.A., Erickson H.P., Kiehart D.P.; Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.; Chain kinase family."; Drosophila stretchin-MicK is a novel member of the Titin/Myosin light chain kinase family."; DMI-12-177(2000).

EMBL, AF257312; AAF90130.1; EMBL, AF254365; AAF90130.1; EMBL, AF264365; AAF90114.1; EMBL, AF264365; Prcalcium—and calmodulin-dependent protein k. .; IDAGO; GO:0004685; Prcalcium—and calmodulin-dependent protein k. .; IDAGO; GO:0004687; Francain-like.

InterPro; IPR007110; IG-like.

InterPro; IPR0071898; Ig-c2.
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STRAIN=CGA009 / ATCC BAA-98;

STRAIN=CGA009 / ATCC BAA-98;

Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J. Harwood C.S.;

"Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Biotechnol. 22:55-61(2004).

EMBL, BX572597; CARZ6936.i. -.

InterPro; IPR009013; Viral_att_shaft.
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                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterayera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophiliae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 18; DB 2; Length 215; 57.1%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA; 24254 MW; E6A8019E1983E9FC CRC64;
                                                                                                                                                   Last sequence update)
Last annotation update)
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PROSITE; PS50835; IG_LIKE; 2.
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OrderedLocusNames=RPA1494;
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Matches 4; Conservative
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110 ISASAEF 116
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                                                                                                                                                                                                  Name=Strn-Mlck;
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STRAIN=VPI-5482 / ATCC 29148;

STRAIN=2550858; Pubmed=12663928; DOI=10.1126/science.1080029;

MEDLINE=25550858; Pubmed=12663928; DOI=10.1126/science.1080029;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).

EMBL: ABO16944; AAO79438.1; -.

Complete proteome; Hypothetical protein.

SEQUENCE 219 AA; 25376 MW; SBDCE2094E688E55 CRC64;
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
OrderedLocusNames=BT4333;
Bacteroides thetalotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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Corynabacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium "Complete genome sequence of the oral pathogenic bacterium G.D. Bacteriol. 185:5591-5601(2003).

EMBL; AE017178; AAQ66820.1; -...
TIGR; PG1823; -...
Complete proteome; Hypothetical protein.
SEQUENCE 217 AA; 23686 MW; DA473C25FF8851DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                          h 81.8%; Score 18; DB 2; Length 217; Similarity 57.1%; Pred. No. 3.7e+03; 4; Conservative 0; Mismatches 3; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Matches 4; Conserv
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Gaps
replacements responsible for the thermostability of Corynebacterium
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                                                                                                                                                                         PROSITE; PS50206; RHODANESE 3; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 219 Aa; 23127 MW; BE96467A6760F332 CRC64;
                         efficiens.";
Genome Res. 13:1572-1579(2003).
EMBL; AP005214; BAC16865.1; -.
InterPro; IPR001763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00450; RHOD; 1.
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